

CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA TCCGAACCCG CTGACCCnAC 360
 CnGCGTGCAA AGCAGGCGCT CTACCCAGCT TGAGCTAAGG 400

(2) INFORMATION FOR SEQ ID NO: 3943:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3943:

CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 60
 TTAAGCCCCT GTCGGTTTTT AAGACCGATC CCTTAGCCG GACTTGGGTA TTCCTCCAAA 120
 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG GTTATGGAGC CGTTAGCTCT 180
 GAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA 240
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 300
 CGCCTTATAT AGTTTGTAAG TnAnnATGGT GGGAGACTAG CGGGGTTCGA ACCGCTGGAC 360
 CTCCTGCGTG CCAAAGCAGG CGGCTTCTAC CCAGCTGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3944:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3944:

CCAAAATTGC ACCTTGTCGT TTATTCGGAA AATCAATATn GnTAGGGGGT ATAAGATGCA 60
 CCTACTTTAA CTGTCGCCAA CATCGCCGCA ATCATTTCAA AACTACGTTC TGTAACAAG 120
 GCAACCCGTT GACCATTGCC CACACCATT TATAGGAGCA TGTGCGCAAT GGCATCCACA 180
 TAGTTGCGTA ATGTTTCATA CGTCATTGTC AAATCATTCA TGA TAGCGC AACATGATTA 240
 CCTTGTCGTG AGAAACTTCA TTAAAGTAAC TTATGAAGA TTTATTTCCC GGGACATTAA 300
 GCATTCGATC GTTAACATGC GTATTGACCC AATTTAGAAG TTCCTCCGTG CCGTTTGGTA 360
 TATCACAAAT TTGTAGTGTA wCtTGaTGCT TCmAAATAtC AATCAn 406

(2) INFORMATION FOR SEQ ID NO: 3945:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3945:

CAATGACAAC AGCAACTGAG ACAGTGTC	60
AAATACCGCAT TAAATGTACC AACTAAAACA AATGAAAATG GTTCAGGAGG ACATCTAACT	120
TTAAAGGAAA TTCAAGAAGA TGTTTCGTCAT TCTTCAAATA AACCAGAGCT AGTTGCAATT	180
GCTGGAACCA GCATCTGAAT AGACCGAAAA AGAGAAGTTA GACGTGCGGC ACCGGCAGAT	240
CCTGAATGCC AACTCCAGCA GATCCAGCGG CTGCAGCGGT TAGGAAACGG TGGTGCACCA	300
GTTGCAATTA CAGCGCCATA TACGCCAACA ACTGATCCTA ATGCCATGAn GCCAGGACAA	360
ATGGCACCTA ACGAnGCTTG TTCATTTGAT GGACAnGGTA	400

(2) INFORMATION FOR SEQ ID NO: 3946:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3946:

CTCGCTGCGA TAAAGTACCA GTTCATAGCA AC TT TGTnT TAATAGGnTC TGAAACGATA	60
CGTGTTGCCG GTTCTGTAAA TGAATAGACC AAAGCATCTT GCATACCAAC AACTATATTT	120
GCTGCAAATC CTCCAACAGC GGAAnATATG CCATCGTTAG TCCAGCGATA GGGTGATAGC	180
CAATTTTAAT AAAAAGCATT GCTGCAACGG CCGGCAAGAT AATTGTCGCA GCATCGCO E	240
CTGTACTACC TAAAATACCA ATTAATATAA TAGTCGGTAA AATTAAGAAA CGTGGTGC	300
GATTCACAAC AGAAATCATT AACTTATCGA AGTATCCTGT TTTCTCTGCA ACACCAATAC	360
CAATCATCAC TGCTAGGTAC TAAGCCTAAT GCTGGGnACT	400

(2) INFORMATION FOR SEQ ID NO: 3947:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3947:

GCCGGCCAGA GGA CT TGGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT	60
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GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCG AACCGCCGAC	120
CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT	180
GGCAACGTTT TACTCTAGCG GAAnTAATTC GnACACCAT CGACGCTAAG GAGCTTAACT	240
TCTGTGTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG	300
TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGChTTCG CAAAACATTT	360
A	361

(2) INFORMATION FOR SEQ ID NO: 3948:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3948:

TTCCGTCAGA CCCTGACATG GTTCATGGGT TCATATTGCA TAGGACCGAA ATCTTCAAAC	60
ACTACGTGCT TTGGGCAGAC TTCGCAAAAA TACGGCCTCA ACAAAGGAAT TAAGCCTCGC	120
ATAAAGCGGA TTTCGAGTAC AGGGAACCGC TACCTCCCCA CCTAGCACGG CAAGATATAT	180
ATTACTATAT TTTAATAGTT AATTGCAAGT ATAAATCATT TATATCATTG TTTACTTTAT	240
ACGACGTCTT GAGAAGTCAT TAATTTAAAT TCATTTGCAA GATGTTTTGA AATATTATAT	300
TGAAACGGCA TTGTATTTTC TAAATACACA nTACTTCGAA CTGTTGChGA ATAGGCCACC	360
GATACATCAC CAACAATTGG nA	382

(2) INFORMATION FOR SEQ ID NO: 3949:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3949:

GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA	60
GACCTTGCGG TCTCAATGCG GTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT	120
AGCGGAACGT AAGTTGGCTA CCATCGACGC TAAGAACCTT TCTTGACTTG TGACAATGC	180
TTGCTTCTTT CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG	240
CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG	300
TTTGCTTTTT AnTTTGACGT TTTAGACATA AAAAAAAGAG ACCTTGCGGn CTCAATGnGG	360

GCTCATCGCA TCCAATTTTT GGCCTGGCAA CGGTTCTACT

400

(2) INFORMATION FOR SEQ ID NO: 3950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3950:

ACTCGGTTTT GCTTGGA AAA TCTATATTTA CTTACTTATC TAGTTTTCAA TGTACAATTT	60
CTTTTTAGTC AAGCGCTCGC ATACTGCTTT ATTTTCATAA GCAATATCAC TTTAACCAAA	120
AAATATTTGA ATGTTAAATA AACATTCAAA ACTAATACA ATATGTCACG TTATTCCGCA	180
TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC	240
CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC	300
TCCTAAAAGG nTACnCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGCGE	360
GTGTACAAGA CCCGGGAACG nATTCACCG	389

(2) INFORMATION FOR SEQ ID NO: 3951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3951:

AAAGCTCGAC TTGTTTACGA TGTTGAAAAA CAAGATTATG TACCTGTATC GCAACCACAA	60
TTACCAATTT TAAATGAATT TAATAAAGAC TTAGTGCATA ACCTTGATAC CATATTCAAT	120
GCGCAAGACG AnCGGGACTA TTTTATGGG AGACATTACG TAATAATTTT TATTACTCTG	180
CTATCAATGT ACCTAAAGCT ACCGATGATT TCCGAGACAT AGACCGTGCG CTTGTCTGGG	240
GGTTCAACTG GAACTTGGT CCATTCCAAT TATGGGATGC AATGGGATAC GAACGTGTTA	300
AAACAnTGAT GGGAAGACGA ACTTGGGAGA CTTACACAA TGGGATTAGT GAnTTAGATG	360
GTGGCTTTAT AAACAAG	377

(2) INFORMATION FOR SEQ ID NO: 3952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3952:

```
CAAAGGGCAG CGAAACCGCG AGTCCAGAGC AAATCCCATATA AAGTTGTTCT CAGTTCGGAT      60
TG TAGTCTGC AACTCGACTA CATGAAGCTG GAATCGCTAG TAATCGTAGA TCAGATGCT      120
ACGGTGAATA CGTTCCCGGG TCTTGACAC ACCGCCGTC ACACCACGAG AGTTTGTAAC      180
ACCCGAAGCC GGTGGAGTAA CCTTTTAGGA GCTAGCCGTC GAAGTGGGAC AAATGATTGG      240
GGTGAAGTCG TAACAAGGTA GCCGTATCGG AAGGTGCGGC TGGGATCACC TCCTTTCTGA      300
AGGATATATT CGGGAACATC TTCTTCAGAA GAGCGGGAAT AACGTGACAT ATTGTATTCA      360
GnTTTGGAAAT GTTTnnTTAA CATtnCAAAA AAATGGGGCC      400
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(2) INFORMATION FOR SEQ ID NO: 3953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3953:

```
TGATTTTGAC GTTTtagACA TAAAAAAAG AGACCTTGCG GTCTCAAATG CGGCTCATCG      60
CATCCATTTT TTGCCTGGCA ACGTTCTACT TAGCGGAAC GTAATTGGCT ACCATCGACG      120
CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTTCTT CGGCTCTCGC      180
TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG      240
TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTGCTTTT TATTTTGACG TTTTAGAAT      300
AAAAAAAAGA GACCTTGCGG TCTCAATGCG GGCTCATCGC ATCCATTTT TGCCTGGCAA      360
CGTTCTACTC nAGCGGGAAG TGAAGnCGGA CTGACCAAGC      400
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(2) INFORMATION FOR SEQ ID NO: 3954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3954:

```
AAACTACATA ATGAAAATGC CGTTTTAATC GGTAAATTAA ATATGGATGA GTTTGCAATG      60
GGTGGTTCAA CAGAAACATC TTATTTCAAA AAAACAGTTA ACCCATTTGA CCATAAAGCA      120
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GTGCCAGGTG GTTCATCAGG TGGATCTGCA GCAGCAGTTG CAGCTGGCTT AGTACCATTT	180
AGCTTAGGTT CAGACACAGG TGGTTCAATT AGACAACCGG CTGCATATTG TGGCGTTGTC	240
GGTATGAAAC CAACATACGG TCGTGTATCT CGATTGGAT TAGTGCTTTG CATCTTCATA	300
GACCAAATTG GGCCATGACT CGAATGTAAA GTAATGCCAT CGTATTAGAA GCTATTCTGG	360
TGCAGATGnT AATGACTCTA CCAGTGCACC AGTGATGAGG	400

(2) INFORMATION FOR SEQ ID NO: 3955:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3955:

TCGATTGGCA TTTCTCCGCT ACCCTCAGTT CATCCGCTCA CTTTCAACG TAACGGTTC	60
GGTCCTCCAT TCAGTGTTAC CTGAACTTCA ACCTGACCAA GGGTAGATCA CCTGGTTTCG	120
GGTCTACGAC AAATACTAAA CGCCCTATTC AGACTCGCTT TCGCTACGGC TCCACATTTA	180
CTGCTTAACC TTGCATCAAA TCGTAACTCG CCGGTTTCATT CTACAAAAGG CACGCCATCA	240
CCCATTAAACG GGCTCTGACT ACTTGTAAGC ACACGGTTTC AGGTTCTATT TCACTCCCCT	300
TCCGGGGGTG CTTTTCACTT TTCnCTTCAA GGTATGGGTT CACTATCGGT nACTAGAGAG	360
TAATTAGCTT AGGnGATGGT CCTCCCAGAT TCGGAAGGGA	400

(2) INFORMATION FOR SEQ ID NO: 3956:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3956:

GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG AACCGGTAGT	60
GGnTnCACTC ACCGCAGATT TTAAGTCCTG TGCGTCTGCC AGTTCCGCCA CCCCGGCACT	120
ATAAAAATGG AGCAGAAGAC GGGATTTCGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT	180
TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCTAAG	240
CTTAGGATCC TAAGTCTAGT GCGTCTGCCA ATTCCGCCAC ACCCGCAAAT GGTGAGCCAT	300
AGAGGATTTCG AACCTCTGGA CCCTCTGGAT TAAAAGTCAG ATGCTCTACC AACTGGAGCT	360

AATGGCTCTT TCCATGGTGC CGGGCCAGAG GACTTTGAA_n

400

(2) INFORMATION FOR SEQ ID NO: 3957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3957:

CAGACATGTG TTATACGGGA AATTGGGCGA ACCGCAACTA TTATACATTG ATTTACACCT	60
TATACATGAA GTTACTTCTC CTCAAGCATT TGAAGGACTT AGGCTTCAAA ACAGAAAATT	120
AAGACGCCCCA GATTTAACAT TTGCAACACT CGATCACAAT GTTCCTACTA TTGATATATT	180
CAATATTAAA GATGAAATTG CAAACAAACA AT CACAACA TTACAAAAAA ACGCCATAGA	240
TTTTGGGGTG CATATTTTGG ATATGGGTTC TGATGAACAA GGTATTGTTC ACATGGTAGG	300
ACCTGAGACA GGACTTACAC AGCCTGGC _n A GACCATCCGT nTGTGGGTGA CTCTCACACA	360
GCCACACATG G _n GCCTTTT	379

(2) INFORMATION FOR SEQ ID NO: 3958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3958:

TGTTAAAATA CGGTACATCT AAATTAATGT TAACTGATTT TCAAAAAGAG AATTAAATAA	60
ATATATTCAA GGTCAG _n AC AACGCGTGAT ATTTGAAAAT GGCCATTTTG TCTAATTGAT	120
AGTGAATATA ATTAGAGTAA GAGGCTGGGA CATAAATCCC TAAAAAACAG CAGTAAGATA	180
ATTTTCAATT AGAAAATATC TTA CTGCTGT TCTCTATTTA TACAATACTT CGTATTGAAT	240
GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT GCTCCCTCAG	300
GGGTCTCGCC ATTAATACTA CGTATTAAACA TGTAATTTTA CTTTGGAAAT ACT _n TAAAAA	360
AATAAGACAT TTG _n CCAACT TGACACTACC AT _n AAAACT	400

(2) INFORMATION FOR SEQ ID NO: 3959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3959:

GAGCCGCAGT GGAATGAGGC CCAAGCGACT GTTTATCAAA AACACAGGTC TCTGCTAAAC	60
CGTAAGGATG TGTTATAGGG GCTGACGGCT GCCCGGTGCT GGAAGGTTAA GAGGAGTGGT	120
TAGCTTCTGC GACGTACrGA ATCGAAGCCC CAGTAAACGG CGGCCGTAAC TAAACGGTC	180
CTAAGGTAGC GAAATTCCTT GTCGGGTAAG TTCCGACCCG CACGAAAGGC GTAACGATTT	240
GGGCACTGTC TCAACGAGAG ACTCGGTGAA AATCATAGTA CCTGTGAAGA TGCAGGTTAC	300
CCGCGTACAG GACGGAAAGn CCCCTGGAGC TTTACTGTAG CCTGATATTG AAATnCGGCA	360
CAGTTTGTAC AGGATAGGTT AGGAGCCTTG GAAACGTGTG	400

(2) INFORMATION FOR SEQ ID NO: 3960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3960:

TGGTCCCAAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA	60
TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG	120
GGCGCATATG TTTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTGAnTnC	180
ACTCACCGCA GATTTTAAGT CCTGTGCGTC TGCCAGTTCC GCCACCCCGG CACTATAAAA	240
ATGGAGCAGA AGACGGGATT CGAACCCGCG ACCCCAACCT TGGCAAGTTG TTATTCTTAC	300
CGCTGGAAct ACTTCTGGCA TATGCGGGTT GAAGGGGAGT CGAACCCCCA CGCTTAGGC	360
TTAAGATTCC TGAAGTCTAG TGCGTCTGGC CAATTTCCGG	400

(2) INFORMATION FOR SEQ ID NO: 3961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3961:

TTTTGATACA TAATCTAAAT TTCTCAAAGC GCCAATAACA GAGGACCATC TCCTAAGGCT	60
AAATACTCTC TAGTGACCGA TAGTGAACCA GTACCGTGAG GGAAAGGTGA AAAGCACCCC	120

GGAAGGGAGT GAAATAGAAC CTGAAACCGT GTGCTTACAA GTAGTCAGAG CCCGTTAATG	180
GGTGATGGCG TGCCTTTTGT AGAATGAACC GGCGAGTTAC GATTTGATGC AAGGTTAAGC	240
AGTAAATGTG GAGCCGTAGC GAAAGCGAnG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA	300
GACCGGAAAC CAGGTGATCT ACCCTTGGTC AEGTTGAAGT TCAGGTAACA CTGAATGGAG	360
GACCGAACCG ACTTACGTTG AAAAGTGAGC GGATGAACTG	400

(2) INFORMATION FOR SEQ ID NO: 3962:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3962:

TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTn CGACCCCTTG GTCCCAAACC	60
AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAnTTAAC GCGCCCGATA GAGTCGAAC	120
CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTG	180
TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAnAAAT GGATCAGAAG	300
ACGGGATTCG AACCCGCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACACTT	360
C	361

(2) INFORMATION FOR SEQ ID NO: 3963:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3963:

CGCGAAATAT CATTTTGAGG AATTCTAACA GAAGTTTTTA TTGGTAGTGT AAGTTGGGCA	60
AAGTGCTCTA TTTTTTTAAA GTATTTCAA GTAAAATTAC ATGTTAATAC GTAGATTAAT	120
GGCGAGACTC CTGAGGGAGC AGTGCCAGTC GAAGCCGTAG GCTGAGACGG CACCCTAGGA	180
AAGCGAACCA TTCAATACGA AGATnTnATn AAATAGAGAA CAGCAGTAAG ATATTTTCTA	240
ATTGAAAATT ATCTTACTGC TGTTTTTTAG GGATTTATGT CCCAGCCTCT TATCTAATT	300
ATATTCACTA TCAATTAGAC AAAATGGCCA TTTTCAAATA TCACGCGTTG GTTTCTGACC	360
TTGGAATATA TTTAT	375

(2) INFORMATION FOR SEQ ID NO: 3964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3964:

AAAATGGCCT TGATAGACTT GCTCAATGCA GGGTTGCCAC AAACCAATGA TGCACTTACA	60
ATTTTAAATA GATTTTAAAG ACCTTGTTGG TTTTGTACAA TTAATGTGAC ATGACTAGGT	120
CTTGACGTT TATATGCATC TTCATTACTG AGTTTTTTGT TGATTTCGTT ATGATTTAAT	180
ACGCCTAATT CTTTCATTTG TTGAACCATT TTTATGAAAA TGTAAGCTGT TGCTTCTGTA	240
TCATAAATGG CACGGTGATG TTGCGTTAAT TCTACGCCAT ATTTTTTAGC CAAGAAATTC	300
AAACCATGTT TACCATATTC AGTATTAATC GTACGAGGAT AATCTAAAG TATCGATAAC	360
ACCATTTCGTT GGATGGTCCA AACCCAAGAC GTTCATATCC	400

(2) INFORMATION FOR SEQ ID NO: 3965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3965:

ACTTTTAATT TTGTCATGAT GTGCCTCCTT ACCGTATGAT GTTATTCAAAGTAAATTGCT	60
TTGCCTGATT TTGCAGACTG ATAAATCGCT TCAAGAATTT TTGTAACCTAC CATTGCTTGT	120
TCCGGTTTCA CAACTGGTTC AGTATCATTT ACAACTGCAT CAATCCAAGC TTTTGCTTCT	180
TCTTCAGCTT CATCCACTTC ATTACCTTCA TAAAAGTCGA CGCCTTGT TTCCAATTCA	240
ACGTGTTTGG TATAAAGTGT ACCCATGTCT TCACCATGAA TACGTAGACC ATCTTTCATA	300
TCAGCACCTG CTTTAGGTTT CTGATAATGA ACATTTTGGC CTCATCCACT TCTAAAnGAA	360
TTAATCGCCC AAGnGGGATT CCAAAAAGGA n	391

(2) INFORMATION FOR SEQ ID NO: 3966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3966:

CGCTATCAGG TATTGTTTCA ACAATTTCAT TAACATATCG TGAAATATCA TTTTGAGGGA	60
TTCTAACAGA AGTTTCTATT GGTAGTGTAG TTGGGGCATG TTATAATTTT TATACATAAG	120
GCACCTCGTT AATTTAGTTT AGTGGTATTT ATTAAATTAT AAGAAGGGAC CCAACACAGA	180
AAATTCATTT TATTGAATTT TACATTTATG TGCAAGTTGG GCAAAGTGTC TATTTTTTTA	240
AAAGTATTTT AAAGTAAAT TACATGTTAA TACGTAtATA ATGGcGAGAC TCCTGAGGGA	300
GCAGTGCCAG TCGAAGcCAA GGCTGAGACG GCACCCtAGG AAAGCGAcnC ATTcAATACG	360
AAGATTGTAT AAATAGAGAA CAGCAGTAAG ATATTTTC	398

(2) INFORMATION FOR SEQ ID NO: 3967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3967:

GCTATAGAAA AAATAAAATC ACAAGTTACG ATTAGCGTAC TTGATGGGGA GTGAAAATAA	60
TGAGAGTAAC AGAGTTATTA ACAAAGATA CAATAGCAAT GGATTTAATG GCAAATGACA	120
AAAATGGTGT TATTGATGAG TTAGTAAATC AATTAGACAA AGCAGGTAAA TTAAGTGATG	180
TCGCGTCATT TAAGGAAGCG ATTCACAATC GAGAATCACA AAGTACAAC TGGTATCGGCG	240
AGGTATTGCC ATTCCACATG CCAAAGTGGC CGCAGTTGAA GTCACCAGCT ATTGCGTTTG	300
GTAAATCTAA AGCAGGCGTG GATTATCAAn TTTGGnTATG CAACCAGCAC ACTTnTTCTT	360
TGTGGTTGGC AGCG	374

(2) INFORMATION FOR SEQ ID NO: 3968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3968:

ACCCCGGCAC TATAAAAATG GAGCAGAAGA CGGGATTCTGA ACCCGCGACC CCAACCTTGG	60
CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC	120
CACGCCGTAA nCTGAGGATC CTAAGTCTAG TGCGTCTGCC AATTCCGCCA CACCCGCAA	180

TGGTGAGCCA TAGAGGATTC GAACCTCTGG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC	240
AACTGAGCTG AATGGCTCTT CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTGACT	300
GGATTACAAG TCAGTTGCTC TACCAATTGA GCTAAGGCCG GGCAATATGT AAGAATAAAT	360
GGTGGAGAAT GACGGGTTTC GAAnCGCCGA CCCTCTGCTT	400

(2) INFORMATION FOR SEQ ID NO: 3969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3969:

GCGAGTTGGG GTGTGGGCCC CAACATAGAG AAATTGGATT CCCAATTTCT ACAGACAATG	60
CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC ATTAnCAATA ATGTGCAAGT	120
TGGCGGGGCC CCAACACAGA AGCTGACGAA AAGTCATTAn CAATAATGTGCAAGTTGGCG	180
GGGCCCCAAC ACAGAAGCTG GCGGAAAGTC AGCTTACAAT AATGTGCAAG TTGGGGTGGG	240
ACAACGATAA AGTAATACTT TTTCTATAGA AATTAGTATT TCTTATGCAT GAGTTTTACT	300
CATGTATTCC TATTTTAAAG TACACATTAG CTGTGGCTAA TGTTTAAGAC CCACTACATA	360
ATAAATCATT AGTGGCTCTn TATCATTTCT GTCCCACTCC	400

(2) INFORMATION FOR SEQ ID NO: 3970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3970:

GATAAGATCA GCCGAAAATG GATGGTGTTA AGAGCGTTAC TTGGTTTGGC GGTATGCTTA	60
TTTTTAATGG CATTGTGTAC GACACCATTA CAGTTTGTAC TTGTGAGGTT ATTGCAGGGA	120
CTATTTGGTG GTGTTGTTGA TGCATCAAGT GCGTTTGCGA GTGCAGAGGC GCCACTGAKA	180
GATCGTGGAA AGtATTAGGA gACTGCAAAT TCAGTCAGCG CAGGtCTCTT GTGGGGCCAT	240
TAATTGGCGG TGTTACAGCT TCGATATTAG GTTTTAGTGC GTTACTGATG AGTATTGCCG	300
TTATTACTTT TATTGTCTGT ATTTTCGGTG CATTAAATg ATTGAAACGA ECATATGCC	360
AAaATCACAA ACACCAAATA TTAATAAAGG TnTTCGCCGT TCCAnTnCA ATGTCTAAT	419

(2) INFORMATION FOR SEQ ID NO: 3971:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3971:

AAACTTGGGA GACTTCAATA ACAGATTTAG GTTTATCTAA AAATCAGGCA TATAATTTCT	60
TAATTACATC TAGTCAAAGA TGGGGCCTTA ATCAAGGGAT AAATGCAAAT GGCTGGATGA	120
GAACTGACTT GAAAGGTTCA GAGTTTACTT TTACACCAGA AGCGCCAAAA ACAATAACAG	180
AATTAGAAAA AAAAGTTGAA GAGATTCCAT TCAAGAAAGA ACGTAAATTT AATCCGGATT	240
TAGCACCAGG GACAGAAAAA GTAACAAGAG AAGGACAAAA AGGTGAGAAG ACAATAACGA	300
CACCAACACT AAAAAATCCA TTAAGTGAG TAATTATTAG TAAAGGTGAA CCnnAAGGAG	360
GGGTTTCCAn AGTCCGTTAT G	381

(2) INFORMATION FOR SEQ ID NO: 3972:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3972:

GGGTTCAGAA CGTCGTGAGA CAGTTCGGTC CCTATCCGTC GTGGGCGTAG GAAATTTGAG	60
AGGAGCTGTC CTTAGTACGA GAGGACCGGG ATGGACATAC CTCTGGTGA CCAGTTGTCTG	120
TGCCAACGGC ATAGCTGGGT AGCTATGTGT GGACGGGATA AGTGCTGAAA GCATCTAAGC	180
ATGAAGCCCC CCTCAAGATG AGATTTCCCA ACTTCGGTTA TAAGATCCCT CAAAGATGAT	240
GAnGTTAATA GGTTTCGAGGT GGAAGCATGG TGACATGTGG AGCTGACGAA TACTAATCGn	300
TCGAnGACTT AATCAAAATA AATGTTTTGC GACCAAATCA CTTTACTTAC TATCTAGTTT	360
GAATGATAAA TACATCATAT GCTGGnGCCA TACCAAGGGG	400

(2) INFORMATION FOR SEQ ID NO: 3973:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3973:

TCTTTTAATT ACGTAATGGC TTACCAAGTTT TTAACATATG TGCAATTCTT TCATATGATT	60
TTTTAGATTT TAGTAAGTCA ATAAAGCCAA TTTTCTCCAA CGATTGAATG TAACGTTGAT	120
TGATAAATGT ATTTCTTGGT AAATCACCAC CCGCTAAAAT TGTGGCGATA TTTAAGGCAA	180
TATGATAATC ATGGTCGCTA ATAAAATGAC CCCGTCTTTG CGCATCTAAT TGTCCTTGGA	240
TCAATGCTTT GAAGTCTTCA CCTAAAGCGA TATATTGATG TCTAGGATTCGGAATATAGT	300
TTGTTTCTGC TTCATATTTT GCACGTGTGA GCGCAACTTC GACACGnTGG TGCCTGGATT	360
nGAAAATAAA CCGGAnCCnG GGATCCACGG GAAATAACCC	400

(2) INFORMATION FOR SEQ ID NO: 3974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3974:

TGCCATGTTT ACCTTGTTTA AAATCAAGGT TTGTAATGTT TCCTTGTTGTC ACGATAATAG	60
GCGTAATATC ACTCTTTGCA TGATTGCGGA TGTAGTCTAA ATCAAAGTTG ATTAATAAAT	120
CACCTTGTTT AACTTCTTGA CCTTCCTCAA CATGTAAAGT AAAGCCTTCT CCGTTTAATT	180
TAAAGTGTC TAAACCGATG TGGATTAATA GTTCTAAACC ACTATCTGAA TACAAGACCA	240
ATTGCATGTT TTGTTGGGAA AATCATTTGT TACTTTACCG TTGAAATGGT GCACGAACT	300
TCACCTTGTC AnGTTTTTGG ATAGCGATAC CGTCACCCCA TCCATTTTTT TTCGCTGAAA	360
CACTTGGATC AnGGCACTTC TGAATAAATG GTGGTTAACT	400

(2) INFORMATION FOR SEQ ID NO: 3975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3975:

CCTTTGCAGC GCCTCCGTTA CCTTTTAGGA GCGACCGCC CCAGTAAAC TGCCCGCCTG	60
ACACTGTCTC CCACCACGAT AAGnGCGGn GTTTAGAAAG CCAACACAGC TAGGGTAGTA	120
TCCCACCAGC GCCTCCACGT AAGCTAGCGC TCACGTTTCA AAGGCTCCTA CCTATCCTGT	180

ACAAGCTGTG CCGAATTTCA ATATCAGGCT ACAGTAAAGC TCCACGGGGT CTTTCCGTCC	240
TGTCGCGGGT AACCTGCATC TTCACAGGTA CTATGATTTC ACCGAGTCTC TCGTTGAGAC	300
AGTGCCCAAA TCGTTAACGC CTTTCGTGCG GGTGCGAACT TACCCGACAA GGAnTTTCGC	360
TAACTTAGGA CC	372

(2) INFORMATION FOR SEQ ID NO: 3976:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3976:

AGGGAATCGA ATTTTCTTTC TCTCCTnCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT	60
GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC	120
CCCATTTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA	180
GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCTT AAATAACTTA	240
ATCTATGTTT CCACCATTTT TATAAGTCAA ACGCTCACAT ACGGCTTCGT TTTCATTATT	300
TTAAAGCTCA TTTACATAAG TAAACTCTGC TTAAATGAT TTAATCATT GTCTGCTAAA	360
ACGGTTTnTT TTATGAAAAG GTTTGAAACG GGTn	395

(2) INFORMATION FOR SEQ ID NO: 3977:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3977:

TTGGTCCCAA ACCAAGTGCT CTACCAAGCT GAGCTACTTC CCGTATAATT AACGCGCCCG	60
ATAGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG	120
GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTnnTTCA	180
CTCACGCAGA TTTTAAGTCC TGTGCTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT	240
GGAGCAGAAG ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGTTGTT ATTCTACCGC	300
TGAACTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA GGCTTAGATC	360
CTTAAGTCTA AGTGCGTCTG GCCAATTTCC GCCAnACCCG	400

(2) INFORMATION FOR SEQ ID NO: 3978:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3978:

AAGTGGTTAA ATATTATAGA AAACATCAAA GGATGTTAAG AAATACAATT TATTACCCAG	60
CATTTAATAA TGGTGCTATA GAAGGAATTA ATAATAAGAT AAAATTAATC AAGTGAATTT	120
CTTTTGGTTA CAGAAATTTT ACAACTTTA AAGCACGTAT AATGATGATT TTCAGCTTGT	180
ACAAAGGAGA AAAAAAGAAG ACAACCAAGC CCAATAATGG ACTGGCCGCC TAATAATAAA	240
AGCTCTAAAA GTTGTATTTT AAAAATAGTT CTTTAAATTA TATACCCACC ACATTTGGTG	300
GAGGAACCTA AAAAAAGCA CTTCCCAAAA ATGGGAAAGT GCAGTnAGTG GAGCCATAGA	360
GGATTCCGAA CCTCGGACCC TCnGAT	387

(2) INFORMATION FOR SEQ ID NO: 3979:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3979:

TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG TATTCTACCG	60
CTGAACTACT TCTGCATATG CGGGTGAAGG GAGTCGAACC CCCACGCCGT AAnTTAGCAT	120
CCTAAGTCTA GTGCGTCTGC CAATTCCGCC ACACCCGCAA ATGGTnGCC ATAGAGGATT	180
CGAACCTCTG GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTT	240
CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTT CAGTTGCTCT	300
ACCAATTGAG CTAGGCCGn CAATATGTAA GAATAAATGG TGGAGAATGA CGGGTTTCGA	360
ACCGCCGAAC CCTCTGCTTG TnAAGGGCAG ATGGCTCnTC	400

(2) INFORMATION FOR SEQ ID NO: 3980:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3980:

TTACCACGTA TTTAGGTTTC TTTGGTGGCT CTAGATTTGT CCCTATTGTC ACAGCATTTG	60
CCGCAATCTT TTTAGGTGTA TTGATGTTTT TCATTTGGCC AAGCATACAA GCCGGCATTT	120
ATCATGTTGG TGGATTTGTA AGAAAACAG GTGCCATCGG TACTTTTGTT TATGGCTTCA	180
TCTTAAGATT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTA CT TACCG TTTTGGCAGA	240
CGGCACTTGG TGGTACTTTA GAAGTCAAAG GGCAC T TAGT TCAAGGTACG CAGAACATCT	300
TCTTTGCTCA ACTTGGTGAT CCAGATGTGA CGAnTATTAT TCCAGGT EG TCACGCTTTA	360
nGTCAGCCGT TTTAATACGA GGATGTT CGG CTAnGTGGTG	400

(2) INFORMATION FOR SEQ ID NO: 3981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3981:

CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC	60
GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG	120
CTGGA ACT TA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GATACAATTC	180
AAGTTGTTGC AACGCAAGGG AAGCGGAGAG ACAGTGTAGT GGATGGAGCA ACGTATAGTT	240
GGATTT CACA GTTGTCGCAC CACAACCGAA CCAAGCGACT GACTGAAGAT TTGGCAAAAT	300
GGnCATATTG ATATCAGGCC TAA GA nTCC ATTCAGGACA TTTAATTAAT CCAACTCAAG	360
CAATGGATAT TGCTTGACAC TGAAAAATGG GTAA n TGGTG	400

(2) INFORMATION FOR SEQ ID NO: 3982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3982:

TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA	60
TAATGTT CAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAA RG CTAG AACAAAGCAA	120
GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT	180
AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG AAAATTATAG GTGTTGAACC	240

TTCAGTGCAA GTAGTATGTA TGAATCTGTT GTGGTAAATA ATCAGGTAGT CACATTGCCT	300
AATATCGATA AATTTGTGGG ACGGTGCATC TGTAGCTAGA GTTGGCGATA TTACATTGGA	360
AATTGCCAAA GAAAAGTAGA GGATTACGTT CCAGTAGAGn	400

(2) INFORMATION FOR SEQ ID NO: 3983:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 390 basepairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3983:

CCACCATTAT TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT TTACCAAGCA	60
AAACCGAGTG AATAAAGAGT TTTAAATAAG CTTGAATTCA TAAGAAATAA TCGCTAGTGT	120
TCGAAAGAcG CGACAAGATT AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG	180
CAGACAATGA GTTAAATTAT TTTAAAGCAG AGTTTACTTA TGTAATGAG CATTTAAAT	240
AATGAAAACG AGGCCGTATG TGGAGCGTTT GACTTATnAA AAATGEGGG AAACATAGAT	300
TCAAGTTATT GAAGGGCGCA CGGTGGGATG CCTTGGGCAC TAGnAAGCCG nTGGAAGGAC	360
GTTACTAACG ACGATATGCC TTGGGGGAGC	390

(2) INFORMATION FOR SEQ ID NO: 3984:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3984:

GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTTGC CTTGTATCTG CAAATGTTTT	60
GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC ACAAATTCAA ATGTATCAGG	120
CGTTTCTTTT ATCCATTTCa ATATATTTCT TTCCGGTTGT ATCGCATAGT ATGTCGCATC	180
TAATTCGACA ACCGGAAAAT GTCCAGCATA TGTTTTAAGT TTATCGGTTT GGCGTTCTAA	240
ATCTTCATAT AATGAATAGT GATCACCCEA ACCTGTTAAT CCGATGTTTT ATCATATATA	300
TCACCAATGT CATCATACCA TATAACTTTT ATCATnATCA TTTCAGCGAA CTTTAGGTTT	360
GnAGGTTTTT TGGCCTGGAT TAAAnATCTT TCGGGCGGAT	400

(2) INFORMATION FOR SEQ ID NO: 3985:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3985:

GCATTTGCTT ATATCTTTAA AAAAGATTTT GAAGATATTG AAGAAAAAC TAAAGAAATT	60
ATTTCTGATA TTGAAAGTAA AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT	120
AAAAAnCAGC AGTAAGATAA TTTTCAATTA GAAAATATCT TACTGCTGTT CTCTATTTAT	180
ACAATACTTC GTATTGAAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTTGGTCTTC	240
GACTGGCACT GCTCCCTCAG GAGTCTCGCC ATTGAATACT ACGTATTAAC ATGTnAATTT	300
TACTTTGGAA ATACTTTTAA AAAATAAGAC ACTTTGCCCA ACTTGGCACA TAAATGTTAA	360
AATnCAATGA AATGAATTTT CTGTGTTGGG TCCCCTnCTA	400

(2) INFORMATION FOR SEQ ID NO: 3986:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3986:

TTCGTTCAAA GTCATCTAGG TCACATTATT CTATTTGGGA TTCTTAGTGC TGTTCCTATT	60
TGCGGCTTTA ACGTCATCTA TTTCTTTATT AGCAATTAAA TGTTTCTAAC TTCACGAAGA	120
ATGACAATAC AAAACGTAAA AAAGTCGCAG TGATCGGTAG TATTTTAGTA TTTATCATTA	180
GTATTCCAGC AACCTTATCT TTTGGTATCT TAAAAGATGT AAGTCGGT GCGGGAACGA	240
TTTTTGATAA TATGGATTTC ATCGTTTCGA ATGTATTGAT GCCATTAGGC GCATTAGGTA	300
CTACGCTTGT CGTAGGnCAA TTATTAGnTA AAAAATTATT ACAnCAATAT TTTGGTAAAG	360
AnCGATTTAG GATTATTCAG TGGTTGGTAT TACTTAATTA	400

(2) INFORMATION FOR SEQ ID NO: 3987:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3987:

GGATTCGAAC CCCC GCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC	60
CGGACTTGGG TATTCCTCCA AAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA	120
CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC	180
TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC	240
TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAA TAATATGGTG GGGACTAnCG	300
GGATCGGAAC CGCTGGACCT CCTGCGTGGC AAAGCAGGCC GCTCTCCCAG CTGGAGCTAA	360
GnCCCCCATA ATAATnACAG TATATCnGGG AAGACAGGAT	400

(2) INFORMATION FOR SEQ ID NO: 3988:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3988:

CAGCTGATAA ACAAGTTGAT CTGGTCCCGA TTTGTTGGGT AAACGGTTGA TTAATGnAAA	60
ATGTTCGCCG AAGGATTCAT AATCCGAGAG GTCTAATTCA ACGTATCATT AATCAAGATG	120
CGCCTATTTA TCAATCTGAA ACAAATTATC ATTCGAAAGA TCGCGGTAAG TCTAAAAATG	80
GTATTCAAAT GGTGTATCAA CATTTAATGA ACGGTGTATC GTTTATGGnT CCTTTTATCG	240
TAGTTGGTGG ACTCCTTATC GCCATCGCGC TGA CTCTAG GCGGTGAACG ACCATCCAAA	300
AGGATTAGTC ATCCAGATG ATTCATTTTG GAAATCCATT GAAAACCATG GGTAGTTTAG	360
CCTTTAAATT AATGGTCCCA TACCAGnCGG GATAAACGCT	400

(2) INFORMATION FOR SEQ ID NO: 3989:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3989:

CCAGAGATTT CCGAATGGGG GAAACCCAGC CATGAGTTAT GTCATGTTAT CGATATGTGA	60
ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA	120
GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCAAACGG GAGAGCCCA AACCAACAAG	180
CTTGCTTnGn GGTnTGTAGG ACACTCTATA CGGATTACAA AGGACGACAT TAGACGAATC	240

ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT CGAAAATGTT GTCTCTCTTG	300
AGTGGATCCT GAGTACGACG GAGCACGTGG AAATTCCGTC GGAATCTGGG AGGACCATCT	360
CCT	363

(2) INFORMATION FOR SEQ ID NO: 3990:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3990:

TTTCCAAGAA CATGAGCCTG TACAGTTAAC ACCATGTnTG nTTCTTACTT CTTTATCGTG	60
GCTCCAACGT TCTCTGTACA TTTTTTCCCA TTCTCTACTT TTTACTTTCTA GGATCGACCA	120
ATTCCCATTA AATTTTTCTG TTGGCTTAAA GAAATTC AAT CCAAATTTTC CCATATTTAT	180
ATCCTCCTAC GTATAAAAAT ACGATGTGTA GATGTCGTGT TTTTAAATAC TTTAAAATGC	240
CCAAGACTAT TGCTTTAATT AGATTGTACA TTTTTTCACA AACATAAAAT ATTAGGGAAT	300
CACCTAATTA CTTAAGGnAT TCCCTATCAA TAACGGGATT TCATGAAAT AATACACAAT	360
CAGTAnGGTC AGCCTAATGC CAGGCTAAAT CGTTCAAATT	400

(2) INFORMATION FOR SEQ ID NO: 3991:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3991:

AAAGTGGTTA AATATTATAG AAAACATCAA AGGATGTAA GAAATACAAT TTATTACCCA	60
GCATTTAATA ATGGTGCTAT AGAAGGAATT AATAATAAGA TAAAATTAAT CAAGTGAATT	120
TCTTTTGGTT ACAGAAATTT CAACAAC TTT AAAGCAnGTA TAATGATGAT TTTCAGCTTG	180
TACAAAGGAG AAAAAAAGAA GACAACCAAG CCAATAATG GACTGGCCGC CTAATAATnn	240
GAGCTCTAAA AGTTGTATTT TAAAAATAGT TCTTTAAATT ATATACCCAC CACATTTGGT	300
GGAGAACCTA AAAAAAGCA CTTCCCAAAA ATGGAAAGTG CAAGTAGTGA GCCATAGAGG	360
ATTCGAACCT CTGACCCTCT GATTAAAAGT CAGATGCTCT	400

(2) INFORMATION FOR SEQ ID NO: 3992:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3992:

AGTGTATGGT TATCAAAGAT TTGATACGAC GGTCATTATT ATTACCGTTA TTGTATTAGT	60
CATTATTGTC CAAGTGATTC AAACGCTAGG GAATGTTCTAGCTAGATTCA TACGTnGACA	120
TTAATGATAT ATAGTGAAGA TTTTGAAAGG AATTGATAGA ATGAAAAGAT TGATTGGGTT	180
AGTTATCGTA GCACTTGTAT TAATTAGCAG CGTGTGGTGG TAACAATGAT AAAAAAGTAA	240
CAATTGGTGT CGCATCAAAT GACACTAAGG CTTGGGGAGA AGGTTAAAAG AATTAGCTAA	300
AAAAAGATGG ATnTTGATGT GGGAGATTAA GCACTTCCTC nGGATTACAA TTTACCGGAT	360
TAAAGCCTTn AAATGGATGG TGATATTGAT AATGAATGCC	400

(2) INFORMATION FOR SEQ ID NO: 3993:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3993:

AAGAATTTTC GACATTTATC TCGTAAAGAA AAGTTACAAC AATTGGTTGA TAAGCAATGG	60
TTATCAGAAG AACAATTCGA CATTTTACTG AATCATCCAT TAATCGATGA AGAAGTAGCC	120
AATAGTTTAA TTGAAAATGT CATCGCGCAA GGnGCATTAC CCGTTGGATT ATTACCGAAT	180
ATCATTGTGG ACGATAAGGC ATATGTTGTA CCTATGATGG TGGAAGAGCC TTCAGTTGTC	240
GCTGCAGCTA GTTATGGTGC AAAGCTAGTG AATCAGACTG GGGATTTAA AACGGTATCT	300
TCTGAACGTA TTATGATAGG TCAAATCGTC TTTGATGGCG TTGACGATAC TGAAAAnTnT	360
CCGCCGGCAT TGAGAGCCTT AGA	383

(2) INFORMATION FOR SEQ ID NO: 3994:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3994:

GGTACTATGA TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGCCTTTTCGT	60
GCGGGTCGGA ACTTACCCGA CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC	120
GCCTTTACTG GGGCTTCGAT TCGTAGCTTC GCAGnnAAAC CnACTCCTCT TAACCTTCCA	180
GCACCGGGCA GGCgtCACCC TGATACATCA CTTACGGTT TAGCAGAGAC CTGTGTTTTT	240
GATAAACAGT CGCTTGGGc TATTCAGTGC GGCTCTTCTG GGCgTTAACC CTGAAAGAGC	300
ACCCCTTCTC CCGAATTACG GGGTCATTTG CCGATTCTT AACGAGATTC GCTCGCTCAC	360
CTTAGA	366

(2) INFORMATION FOR SEQ ID NO: 3995:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3995:

AGATATTTTA CATGTGAATC AAGTAGGTAT TCATGATAF TTCTTTGAAT TAGGTGGCCA	60
TTCATTAAAA GCAACGTTAT GnTGAATCGG ATAGAGGCAT CTA CT GGGAA ACGATTACAA	120
ATTGGTGATT TATTACAAAA GCCAACTGTA TTTGAACTAG CACAAGCGAT TGCTAAGGTT	180
CAAGAACAAA ACTATGAAGT GATTCCAGAA ACTATAGTTA AAGATGATTA TGTGCTGAGC	240
TCTGCACAAA AGCGTATGTA TTTATTATGG AAATCAAACC ATAAAGATAC GGTGTATAAC	300
GTACCTTTTT TATGGCGGTT ATnCATCAGA ACTTAATGTA GCTCAnTGCG ACAAGCATG	359

(2) INFORMATION FOR SEQ ID NO: 3996:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3996:

CAATTATTGG TATTCAACTT AAAGATCATG ATGATTTAAT ACAACTCAAA CAACGTTnAA	60
ATCATTTTGA TCCTTCCAAT ATTTATATTA ATGAAAATAA GATGTTATAT TCATTGTTAA	120
TTTAACACAT AGTAAGAAAA ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC	180
TGCTTTTTTAT TATACTTTAC ATTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA	240
AGCCATCTTT CTTTGTGTTT GCTTTTATTT TGACGTTTTAGACATAAAAA AAGAGACCTT	300
GCGGTCTCAA ATGCGGCTCA TCGCATCCAC TTTTGCCTG GGCAACGTTC TACTCTAGGC	360

GGAAAnGTAAG TGGGACTTAC CATCGACGGn TAAGGGGCTT

400

(2) INFORMATION FOR SEQ ID NO: 3997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3997:

GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC TTATCGTGGT GGGAGACAGT	60
GTCAnGCGGG CAGTTTGA CT GGGGCGGTCG CTCCTAAAAG GTAACGGAGG CGCTCAAAGG	120
TTCCCTCAGA TGGTTGGAAA TCATTCATAG AGTGTAAGG CATAAGGGAG CTTGACTGCG	180
AGACCTACAA GTCGAGCAGG GTCGAAAnCG GACTTAGTGA TCCGGTGGTT CCGCATTGAA	240
GGGCCATCGC TCAACGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG	300
TTACACACGAC GGGGAGGTTT GGCACCTCGA TGTCGnCTCA TCGCATCCTG GGGCTGTA	358

(2) INFORMATION FOR SEQ ID NO: 3998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3998:

TAGGAGGAAT TTATATGACA TTTGAAAAAG AAACGGTCTT AAAAACATTA TTTCCTGAAG	60
ATGTACTTAG TATTGCTAAA GGTTTAACAG ACGGTGAGT CGAATTTTTA CAACAAGTAG	120
ATTCATTGCT AGAAAGTAAG TACCGTGAAA ATATTAATCA ACATTGGATA GACGCTACTG	180
TACCCGAGGA CTATTTTAAA GATCTGGGAG ArTTAAATTA TTTTAACArT CCATTACTTT	240
ACAAGGATCG TCCAAACGCC AAAATGCCTA GTCAnCTATT TCAGTTTTTC ATGTCTTACC	300
TACTCGCGCG ATTTGATATT TCCTTAGCTA CCCTACTCGG TGTTACCAA GGTTAGGGCA	360
TAACACTTTC TATTTGCGAG GTAGCAAAGA CAAATTGCGA	400

(2) INFORMATION FOR SEQ ID NO: 3999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3999:

CGCCCCTTAG TGCTGCAcTA ACGCATTAAAG CACTCCGsCT GGGGAGTACG ACCGCAAGTg	60
AAACTCAAAG GAATTGACGG GGACCCGCAC AAGnGTGGAG CATGTGGTTT AATTCGAGGC	120
AACGGtAGAA CCTTACCAAA TCTTGACATC CTTTGACAAC TCTAGAGATA GAGCTTTCCC	180
CTTCGGGGAC CAAAGTGACA GGTGGTGCAT GGTGTGTCGTC AGCTCGTGTC GTGAGATGTT	240
GGGTAAAGTC CCGCAACGAG CGCAACCCCTT AAGCTTAGT GCCATCATTA AGTTGGGCAC	300
TCTAAGTTGA CTGCCGGTGA CAAACCCAGG AAGGTTGGGG ATGACGTCAA ATCATCATGC	360
CCCTTATGGn TTTGGGTTAC ACAAGTGGTT ACAATGGG	398

(2) INFORMATION FOR SEQ ID NO: 4000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4000:

TGTTCTTGCA ACGCTATTTA GTATCAGGTT TAACAACAGG TGCGACAAAA GGTTAGTTT	60
AAATTAGGAG TGGGGCAGAA TTGATAAAGA ACCACTAATG ACGATAAAGA TTAAAAGGAG	120
GACGTTATGA TGACGATTAA AGTTGGAATC ATTGGGTGTG GTGGTATTGC GAATGGCAAG	180
CACATGCCAA GTTTACAAAA AGTTGAAAAT GTTGAAATGA TCGCATTTTG TGACGTAGAC	240
ATTTCGAAAG CAGCGaGTGC GGCAGAAGCA TACGGAACTG ACAATGsCAA aGtTTATGAT	300
GATTACmAAG CaTTGTtAAA AGATGACACG ATTGATGTTA TCCATGTTTT GTACCCCCAA	360
TGGACCCCGC ATTGTGG	377

(2) INFORMATION FOR SEQ ID NO: 4001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4001:

TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAeTAAG CAACATGTAG GCCGTTGTCA	60
CTTAACttCT TGTTTTTCCG ATGACAGCTT CTATTTAGAG AATGTCATGA TTATTTTATA	120
TTCACttCAA TGTTATCAAT ATTAGTGCCA TCTATGACAT CTGCCATGCG ATTTTCTTGT	180

AATTTTTTGT GCAATTCAAA CGTGACTTT CCACCGTTTT TCATTTTAAT AACAAATTTA	240
CCTGAACCAA CGTTACCGTA CAGATTATTT TTTTCAATAA GTGTTTTCTC AATTTAAAAT	300
CAAGTTCTTT CAAGGAAATC TGTCTTTAG TAATCTTGAA TTCTGAAACA TCATGGGnGA	360
TTGTACCGTA TnATCTTnCC TAGTAAT	387

(2) INFORMATION FOR SEQ ID NO: 4002:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4002:

CTATTACGAT TGCTGCGAAA GAAGGTATTA AAAATATACA AATAGGCATG GCTCACCGTG	60
GACGTTTAAA CGTTTTAACG CATGTCTTAG AAAAACCGTA CGAAATGATG ATTTCAGAAT	120
TTATGCATAC AGATCCAATG AAATTCTTAC CTGAAGATGG TAGCTTGCAG TTAAGTCTG	180
GATGGACTGG TGATGTGAAA TATCACTTGG TGGGCATAA AACTACTGAT TCATACGGTA	240
CAATGCAGCG TATTGCACTG GCTAACAATC CAAGTCACTT GGAAATTGTT GCACCTGTTG	300
TTGAGGGGCG TACGAGAGCA GCACAAGATG ATACACAACG AGCTGGGGCT CCGACGACTG	360
TCCATCATAA AnGCAATGnC CATTGTTGAT ACATGGCGAT	400

(2) INFORMATION FOR SEQ ID NO: 4003:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4003:

AGAAATATAT GCATTTTCGGA TATCATGGTA AAGAGAATGG ATTAAGCGGT AAATCACGTG	60
ATGAAGTGCG AGCGAAATGA AACAAAATTT AGATGTCATG CGAGACGATA ATCAAAGGGA	120
CGACAGGTGA TGGGGTTGAA AGTGTAACn GCTACACTGG TCATGATGCT GCTAAACTAC	180
GTGATTATAA TGAAACACAT CATGCTTTGT CTGGATATGA AATGATTGAC GCAGCAAAGG	240
TGCCATTGCA ACAAATGAAG TCAATGCTGC GATGGGTATT ATTTGTGCAC GCCAACAGCT	300
GGTTCCTCGG GTACCATTCC CGGTGCACTT TTAAATTAG GAAAAAACAC ATGATTTAAC	360
AGAAGAGCAA ATGATTTGAT TTCTTATTCA CTTCAGCAT	400

(2) INFORMATION FOR SEQ ID NO: 4004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4004:

TGAAATAGAA CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC	60
GTGCCTTTTG TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT	120
GGAGCCGTAG CGAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GACCGAAAC	180
AGGTGATCTA CCCTTGGTCA GGTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA	240
CTTACGTTGA AAAAGTGAGC GGATGAACTG AGGGTAGCGG AGAAATTCCA ATCGACCTGG	300
AGGATAnTGG TTCTCTCCGA ATAGTTTAGG GCTAGCCTCA AGTGTGATTA TTGAGGTAGA	360
nACTGTTTGA CGAGGGGCCC TCTCGGGTAC CGAATTCAGG	400

(2) INFORMATION FOR SEQ ID NO: 4005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4005:

ATACTAAGGC GTTATTAGAC GaTTAGACAA TGGTGTGATT AAAGGTGCAG CACTTGATAC	60
GTATGAATTT GAACGCAAAC TTTTCCCAAG TGATCAAAGG GGCAAAACAC TGAACGATCC	120
ATTGTTAGAA TCGTTGATTG ACAGGGAAGA TGTCATTA ACACCACATA TTGCGTTTTA	180
TACTGAAGCT GCAGTTAAAA ATCTAATTGT CGATGCATTA GATGCAACAT TAGATGTATT	240
GGCAGACTGG AGATACTAGG TTACGAGTAA ATTAAAAATC GAACTGATGA GATAATTTGG	300
ATTGTTGGGG ATTCTGCATC CAGTTCGATT TTTTAAATTT GGTGTTGGAT GACGTTGnAA	360
TGTTGCCTAA TTTAAACGAC ATCGTAAACC nTGGATCCTC CAATGGCGTC CTTnC	415

(2) INFORMATION FOR SEQ ID NO: 4006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4006:

CTAACAGAAAG CTAGTATAGG AAATCGGTAC TCGTTAAGGC TGATCTGTGA TGGGGAGAAG	60
ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA AAGCCTCTAG ATAGAAAATA	120
GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG	180
AACTCTCGTT AAGGAACTCG GCAAAATGAC CCCGTAAC TT CGGGAGAAGG GGtGCTCTTT	240
AGGGTTAACG CCCAGAAGAG CCGCAGTGAA TAGGCCCAAG CGACTGTTTA TCAAAAACAC	300
AGGTCTCTGC TAAACCCGTA AGTGATGTAT AGGGGCTEAC GCTGCCCGGT GCTGGAAAGT	360
TAAngAGAGT GGGTTACTTC TTGCGACTTA nCGAAATCGA GnCCCCAGTA AACGGCGGGC	420
CGTAACTATA ACnGTCCTAA GGTA	444

(2) INFORMATION FOR SEQ ID NO: 4007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4007:

TTTGAAC TCT ATCAAAGCAT CAGCAATCAA AACATACGTA TCTTTACAAC AGTAATATG	60
CATTCTATGA TGCTTCTAAC TGAATTAAAG CATCGAACAA TCGGAAGCAT ATTTCTAAAT	120
TATTTATTCA TTATAGTCTT AAACATAACA TGACCTAATA TATTACTAAC CTATTAAAT	180
AAACCACGCA CATCTAAGTG ATATACGACA ATCACAGCAA TAATAATTGC TTTAGAAAGT	240
CGTGCCGAAC TGGAAC TTAGTCTAGTT CGAACACACA CTGATGTGAG TGGTTTTCTT	300
TATTTTAAAC ATGAACAATC AGATAAGTTA CTAGCATTAG CAAATATTAT TAAATCAAGG	360
GCTTCGnTTC ATAAATTTAA AACATGTTAA ATTAGACGTG	400

(2) INFORMATION FOR SEQ ID NO: 4008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4008:

TATACTTGTT TTTACAAACC ACAAAAAGCT CTAAACATTA GTTTAAACCA ATGCTTAGAG	60
CTTTCTAATT ATTTTATGCT TTAAAAGATA CTGTGTTATC TACGATGACC TTACCGTCTT	120

TAATAACTTT TTCTGCGTGA TTGATACCAA AATGATATGG AATATATTCA TGATTTGGTG	180
CATCCCAAAT TACTAAATTA GCCTTATCAC CTGTGTTAAT TGTACCCGCG TTAATGTCA	240
TTGCTTTAGA GCCATTGACC GTAACAGCAT TCCAAACTTC ATTAGGTGAT AGCTTTAATT	300
TCAAGGCTGC AATCGCCATA ACAAGTTGTA AGTTGTTTGT GGACACTACT ACCAGGGTTA	360
TAATCAGTTG GCTAATGCCA TCGGCACCGG TTAATGGTCC	400

(2) INFORMATION FOR SEQ ID NO: 4009:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4009:

ACAAACATTG AAATTAGAGG TATATAAAAA ATGCTTCTGC AATAGATGCA ATAAACATGC	60
AATACAATAT GGAGGCGAAG TAAATGAAAA GTATTACGTT TGAAGAACAT TATGTCATTG	120
AAGATATTCA AAAAGAAACG ATGAATGCGA TATCAGCAGA TCCTAAAGGT GTACCGATGA	180
AAGTAATGTT AGAAGGCCTT GAAAAAAGA CAGGTTTAC AAATGCCGAC GAATTATCAC	240
ATCATGATGA ACGTATCCAA TTTATGAATA ATCAAGACGT TCAAATTCAA GTCTTATCTT	300
ATGGAAATGG TTCTGCTTCA AATTTGGTTG GTCAGAAAGC CATTGAATTA TGTCCAAAAG	360
GCAAATGATC CATTGGGCAA ACTATATTGC ACCATATCCC	400

(2) INFORMATION FOR SEQ ID NO: 4010:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4010:

ACTAGAGAAG GTATGTTACG TGACAAATGAA TTACTAAATG GTATTTATTC ATCGAGTTAC	60
ATCTATAGTT TATTAAAATC AGAATACGAC CAAAATGAC AAATTAGACT TACAAAAGAG	120
TGATGACATT TAAAATGGCA GCGCTCTTTT ATTTAATTTT TGAAAATAAA AGGTTGTTGA	180
CAGTATTATT TTATAACAAT ATAATGATTT TGATAATTAT TATCAACTAG ATGATGTTTA	240
TGGGAGGATG CTTTAAAACA GCCGTTTTAA GTGTAATGTA TTATTTTAGC GTGTAGGGAT	300
GCGAAAATAT ATTTATAGGA CACATCTTGG GGATAATnGA TTTCTATAAT GAGGTGTCAA	360
ATGGAAAAGT TACCACGCTA TTATTAGCCn CCACGTATT	400

(2) INFORMATION FOR SEQ ID NO: 4011:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4011:

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TnTCAATTAG AAAATATCTT ACCGCTGnCT CTATTTATAC AATCCTCGTA TTGAATGGnT      60
CGCTTTCCTA GGGTGCCGTC TCAGCATCGG CTTGCACTGG CACTGCTCCC TCAGGAGTCT      120
CGCCATTAAT ACTACGTATT AACATGTAAT TTTACTTTGA AATACTTTAA AAAAATAGA      180
CACTTTGCCC AACTTACACT ACCAATAAAA ACTTCTGTTA GAATTCCTCA AAATGATATT      240
TCGCGACATG TTAATGAAAT TGTTGAAACG ATACCTGATA GCAAATTCGA TGAATTCAGA      300
CATCATCGTG GCGCAACATC CTATCATCCA AAGATGATGT TAAAAATCAT CTTATATGCA      360
TATACTCAAT CTGTATTTTC TGGTCGTAGA ATAGAGAAAT TACTTCATGA CAGTATTCGA      420
ATGATGTGGT TAGCTCAGGT CCAAACAnCT TCTnATAAAA CTATTAATCG TTTTGGGGTG      480
GAATCCnAAT ACTG      494
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(2) INFORMATION FOR SEQ ID NO: 4012:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4012:

```
TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTACTTTTTT ATTTTGACGT TTTAGACATA      60
AAAAAAGAGA CCTCACGGTC CAACTTGCCT GGCAACGTTC TACTCTAGCG GAAGTAATTG      120
GCTACCATCG TCGCTAAAGA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTC      180
CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT TCTCGTTTC      240
TCAGATTCAA ACGTTTTTCAC TTCGCCAAGC CATTTTTCTT TGTGTTTACT TTTTATTTTG      300
ACGTTTTAGG CATAAAAAAA AGAGACCTTG CGGTCCCAAT GCGGGCTCAT CGCATCCATT      360
TTTTGGCCTG GGCAACGTTC TnATnCCAGC GGAAAnTnAAT      400
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(2) INFORMATION FOR SEQ ID NO: 4013:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4013:

CGAACTGCCG AACCCGAAGA GCGGATTTAC AGTCCGCCGC GTTTACCACT TCGCTACCCC	60
TCCAGCTTAT TCATATAATT TAATAATCAA AATGGTGGAG AATGACGGGT TCGAACCGCC	120
GACCTCTGCT TTGTAAGGCA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGACT	180
CCTACGGGAC TCGAACCCGT GTTACCGCCG TGAAAGGGCG GTGTCTTAAC CGCTTGACCA	240
AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG	300
CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTTA CTCTnAGCGG	360
AACGTGAATT CGACTTACCA TCGACGnTAA GGAGCTTnAC	400

(2) INFORMATION FOR SEQ ID NO: 4014:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4014:

ATTAGGACCT CAAGACGATA TTAATAAATT TGAATACTTA AAAAAATCTT CTCAAATAC	60
AGGTACTTCA TTATTGGTAT TCAACTTAAA GATCATGATG ATTTAATACA ACTCAAACAA	120
CGTGTGAAAT CATTTCGATC CTTCCAATAT TTATATTAAT GAAAATAAGA TGTTATATTC	180
ATTGTTAATT TAACACATAG TAAGAnAAAC AGTCATAAAT TGATTTCTAA TTGAAATCAT	240
CTTATGACTG CTTTTACATT ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTT	300
ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA	360
nGnGACCTGC GGTCTCAATG CGGCTTCATC GCATCCÆTT	400

(2) INFORMATION FOR SEQ ID NO: 4015:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4015:

GAATGAAAAG CTCTAAAAGT TGTATTTTAA AAATAGTTCT TTAAATTATA TACCCACCAC	60
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ATTTGGGGAG GAACCTAAAA AAAAGCACTT CCCAAAAATG GAAAGTGCAA GTAGTGAGCC	120
ATAGAGGATT CGAACCTCTG ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGACT	180
AATGGCTCTG AATGGCTGGG CTAGCTGGAT TCGAACCAAC GAGTGACGGA GnAAAGGTCC	240
GTTGCCTTAC CGCTTGGCTA TAGCCCAATA TATAGATGGT GGAGGGGGGC AGATTCTGAAC	300
TGCCGAACCC GAGGAGGCGG ATTTACAGTC CGCCGCGTTT AGCCCACTTC GnTACCCCTG	360
CCAGnTTATT CATATGA	377

(2) INFORMATION FOR SEQ ID NO: 4016:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4016:

CCCAGAGTTT TnCACGAATA TATGGATATT TGATTCTGAGG ACTGTATTCA TACCAAGAGA	60
ATGACGCACC TGACATCCTC TCGGTTTATA TTCAGGCATA TCCGGACCAC AACTTGGATA	120
GTCAGTTTGT TGATTTTCCC AGGTAATCAC ACATTTTTC ACAAATACTT TCCAAGAACA	180
TGAGCCTGTA CAGTTAACAC CATGTGTGTG TTCTTACTTC TTTATCGTGG CTCCAACGTT	240
CTCTGTACAT TTTTTCCTAT TCTCTACTTT TACTTTCTAG GATCGACCAA TTCCCATTGA	300
AATTTTCTG TTGGCTTAAA GAAATCAATC CAAATTTCCC ATATTTATAT CCTCCTAAG	360
GTGAAAAATA CGGTGTGTAG AnGTCGTGGT TTTTnAAATA	400

(2) INFORMATION FOR SEQ ID NO: 4017:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4017:

CTTTGAGCGC CTCCGTTACC TTTTAGGAGG CGACCGTCCC AGTCAAAGTG CCCGnCTGAC	60
ACTGnCTCCC ACCACGATAA GGGCGTGGGT TAGAAAGCCA ACACAGCTAG GGTAGTATCC	120
CACCAGCGnC TCCACGTAAG CTAGCGCTCA CGTTTCAAAG GCTCCTACCT ATCCTGTACA	180
AGCTGTGCCG AATTTCAATA TCAGGCTACA GTAAAGCTCC ACGGGGTCTT TCCGTCCTGT	240
CGCGGGTAAC CTGCATCTTC ACAGGTACTA TGATTTTACC GAGTCTCTCG TTGAGACAGT	300

GCCCCAAATCG TTACGTCTTT CGTTGCGGGT CGGAATTAC CCGACAAGGA ATTTTCGTTAC 360
 CTTAGGACCT TATAGTTACG GCCGnCTTTA ATTGGGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4018:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4018:

TGTCGATTTA AGAGGCATGC TACGAGGAAT GATTGGTCAT CCGAAAAAAG ATCGAGCGGC 60
 ATATGAGGCA CGCCAAGCGA TTCCAAACAT TAATGAAAAC AGTCCGCCAA TATTATTGT 120
 ACATGGAGGG AAAGACCAGC AAGTTGGTAT TCATCATGCG TATTATTTAG CGGACCAACT 180
 AGAGTTAAAA GGTGCCACGC ATGnAAACAT TTTATCAAAT GGCAGAAGGA CATGTGCCAA 240
 GACCACCAGC GATGGTTGAA ACATTGACTT ATATTAAAGA GTTTATGAAC CAAGTTGAGT 300
 CGCATAGCTT AGTTATGGAA ACGTGGTGTG CGCATGGGGA ACTATTCAAG CTTTGGAGGA 360
 TGTGGTACTT ACATGCGTTG GAATTAGGGG TCCGTTACT 400

(2) INFORMATION FOR SEQ ID NO: 4019:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4019:

GGAGGTTTGG CACCTCGATG TCGGCTCATC GCATCCTGGG GCTGTAGTCG GTCCCAAGGG 60
 TTGGGCTGTT CGCCCATTAAGCGGTACCA AECTGGGTTC AGAACGTCGT GAGACAGTTC 120
 GGTCCCTATC CGTCGTGGGC GTAGGAAATT TGAGAGGAGC TGTCCTTAGT ACGAGAGGAC 180
 CGGGATGGAC ATACCTCTGG TGTACCAGTT GTCGTGCCAA CGGCATTAGC TGGGTAGCTA 240
 TGTGTGGACG GGATAAGTGC TTGAAACATC TTAAGCATGA AGCCCCCTC CAAGATGAG 300
 ATTTCCCAAC TTCGGTTTnT AAGATCCCTC CAAAGnTGAT GGAGGTTTAA TAGGTTTCGA 360
 GGTGGGAAGC AnGGTGGACA GTTGGGAGCT GGACGAnTAC 400

(2) INFORMATION FOR SEQ ID NO: 4020:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4020:

```
GAAGATGTTT GTCATTCTTC AAATAAACCA GAGCTAGTTG CAATTGCTGA ACCAGCATCT      60
AATAGACCGA AAAAGAGAAG TAGACGTGCG GCACCGGCAG ATCCTAATGC AACTCCAGCA      120
GATCCAGCGG CTGCAGCGGT AGGAAACGGT GGTGCACCAG TTGCAATTAC AGCGCCATAT      180
ACGCCAACAA CTGATCCTAA TGCCAATAAT GCAGGACAAA ATGCACCTAA CCGAnTnTTG      240
TCATTTTGAT GACAATGGTA TTAGACCAAG TACAACCGT TCTGTGCCAA CAGTTAAACG      300
TTTGTTAATA ACTTGCCGGG CTTACACTA ATCAATGGTG GGCAAAGTAn GGGTGTTTAG      360
TCATGCAATG GGTAAGAACG AGCATGTTTG GATTTCAGGG      400
```

(2) INFORMATION FOR SEQ ID NO: 4021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4021:

```
CTAAGTCATG AATGGGAAGT GGCTCGCGTT GAAGAAGGAC TGACTACTGC TGCACACAG      60
CTTGCTAAAC AATTATCAGA ATTAGATTTA GCGTCACATC CTTTTGTGAT GTCAGAGCAG      120
TTTGCAAGTn TAAAAGATCG TCCATTTTCT CCATTAGCTA AAGAAAAAAG AGGATTAAGA      180
GAAGCGGATT ATCAAGTGTA TCAAGCTGAA TTAAATCAAT CATTTCTTTT AATGGTTGCA      240
GCAGTTAAAA AGACACATAT GATTCATGGC GATACTGCAA ATATCGATGA ATTAGAAAAT      300
TTGACAGTAC CTATAAAAGA ACAAGCGACA GACATGTAA AATGATCCAA GGTTATCAnT      360
AGATGACTAT GTACCATTCC GGTACnTCCT GGCCAT      396
```

(2) INFORMATION FOR SEQ ID NO: 4022:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4022:

```
GATTGGTCTG nAAGAAGAAT TAATGGAAAA GCTACGTGAA AAATTAGAAG CGGCATTTGA      60
```

TACGATTTAC GAATTGTCTC AAAACCGAAA AATAGATATG AGACTTGCAG CATATATCAT	120
AGGTATTAAA CGTACAGCAG AAGCAGCTAG ATATCGTGGT TGGGCATAAT TAATTATCAT	180
ATGTGATTTA ACGAGCTTGG GACAGAAAAC AAAGCCCTAA GCTCGTTAAT TTTATTTAG	240
CAGTAGTTGA CTGTAAAACA ATGCCCCGTGT AAACGCTCTT TTCAAAAATA GTCGGGGCCC	300
CAACACAGAG GCTGGTGGGA AAGTCAGCCT ACAATAGnGT GCAAGTTGGC nGGGGCCCCA	360
ACACAGAGGC TGGCGG	376

(2) INFORMATION FOR SEQ ID NO: 4023:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4023:

CAAATGGTGG AGCCATAGGA GGATTCGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT	60
CTACCAACTG AGCTAATGGC TCTTCCATGG nGcNggCCAG AGGACTTGAA CCCCCAACCT	120
ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC GGCAATATGT AAGAATAAAT	180
GGTGGAGAGT GACGGGTTCG AACCGCCGAC CTCTGCTTG TAAGGCAGAT GCTCTCCCAG	240
CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTC TACTCTAGCG GAAntAATTC	300
GGACTACCAT CGACGCTAAA GGAGCTTAAC TTCTGTGTTC CGGCATGGGA ACAGGTGTGA	360
CTCCTTGCTA TATCACCAGA C	381

(2) INFORMATION FOR SEQ ID NO: 4024:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4024:

GCCCCTTATG ATTTGGGCTA CACACGTGCT ACAATGGACA ATACAAAGGG CAGCGAAACC	60
GCGAGTCGAA GCAAATCCCA TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC	120
TACATGAAGC TGGAATCGCT AGTAATCGTA GATCAGCATG CTACGGTGGA ATACGTTCCC	180
GGGTCTTGTA CACACCGCCC GTCACACCAC GAGAGTTTGT AACACCCGAA GCCGGTGGGA	240
GTAACCTTTT AAGGAGCTAG CCGTCGAAGG TGGGGACAAA TGGATTGGGG TGAAGTCGTG	300
AACAAGGTAG CCGTGATCGG AAGGTGCGGC TGGGATCACC TCCTTTGCTG AAGGATGATG	360

ATTTCGGnAA CATCnTTCTT CCAGAAGATG CC~~G~~TAATAA

400

(2) INFORMATION FOR SEQ ID NO: 4025:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4025:

CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGGG TGAGAATCCC GTCCACCGAT	60
TGCTAAGGTT TCCAGAGGAA GGCTCGTCCG CTCTGGGTTA GTCGGGTCCT AAGCTGAGGC	120
CGACAnGTAn GGCGATGGAT AACAGGTTGA TATTCTGTGA CCACCTATAA TC E TTTAAT	180
CGATGGGGGG ACGCATAGGn ATAGGCGAGG TGCGATTGGA TTGCACGTCT AAGCAGTAAG	240
GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT	300
GTGTCTTCGA GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AA	352

(2) INFORMATION FOR SEQ ID NO: 4026:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4026:

TGGGGCTCTT CCCGTTTCGC TCGCCGCTAC TAAGGGAATC GAATTTTCTT TCTCTTCCTC	60
CGGGTACTAA GATGTTTCAG TTCTCCGGGT GTGCCTTCTG ATATGCTATG TATTCACATA	120
TCGATAACAT GACATAACTC ATGCTGGGTT TCCCCATTCG GAAATCTCTG GATCAAAGCT	180
TACTTACAGC TCCCCAAAGC ATATCGTCGT TAGTAACGTC CTTCATCGGC TTCTAGTGCC	240
AAGGCATCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA	300
AnGTTAACAT GAAGTTAGGT TCTTTTATAA AAGGATTAAA nGGGTATTA ATCTTGtGnG	360
TGTTCTTTTCG	370

(2) INFORMATION FOR SEQ ID NO: 4027:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4027:

TCATGTTTCG CTTGGTTTAA TGCTGTTAAT GCGTTATCGA CACGATGTTT TTCATCTGAA	60
ATTTGTTGTG CAGTTGCATC GCCATTGTCA ATAACACGTT GAGCTGCAGT TATTTTCAGTT	120
TCTGCTTCCG CTTCTTCGCA TTATAGTTAT CAATACTTTG TTGCGTCATA CCAGCAGTTG	180
ATGGTACTTG GTTCACAGAA CTTTGTAAGT TATTTTTAGA CGTTACTAAT TGGCTATTAT	240
CTTCTTTATT TTGAAGTAAT GCTTTACTTG GATCAATCTT AGTTTGTGCG CACGAACTTT	300
AGTTAGTGCG TGCAGAACT TGTTGTGGTG TTGCACGCTC ATTAATGAAG CACTGTTGGT	360
GCCTCCGTTT TCGCATATG GATTGTTGTT GGCATGAGG	400

(2) INFORMATION FOR SEQ ID NO: 4028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4028:

CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC	60
CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG	120
GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTCGTCAGA	180
TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTAATTTTTA TTTTGACGTT	240
TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC	300
CTGGGCAACG TTCTACTCTA GCGGGAACGn AAGTTGGGCT TACCATCGAC GCTAAGAACC	360
TTTCTTGAC TTGGTGGACA AACGnGTGG CTGCTTTTCC	400

(2) INFORMATION FOR SEQ ID NO: 4029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4029:

AGGACTTGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC	60
GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCG AACCGCCGAC CCTCTGCTTG	120
TAAGGCAGAT GCTCTCCAG CTGAGCTAT TCTCCGATTT AAAACTGCCT GGCAACGTTT	180

TACTCTAGCG GAAnTAATTC GGA	240
CTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTT	
CG GCATGGGAAC AGGTGTGACC TCCTTGCTAT	300
AGTCACCAGA CATATGAATG TAATTTGATA	
CATTCAAAAC TAGATAGTnA AGTGAAAAGT	360
GATTTTGGnT TCGCAAAACC ATTGATTTT	
GATTGAAGTC CTTGATCGA TTGAGTGATT	400
CGTGCAGCTn	

(2) INFORMATION FOR SEQ ID NO: 4030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4030:

GATGATAAAT CATGTTTTTC ATACCAAGTC	60
GCTGCCGGCA AAACAATGTC AGAATATAAC	
GGTGTGCCG TCATTCTGAA GTCTAAAGAG	120
ACCACTAAAT CTA	
ACTTACC TGTTGTTTCT	
TCACGCCACG TAATTTCTTC TGGCTTTTCA	180
TCTTCATTTG GTGTAGCTAA TAACCCTGAT	
TTTGTGCCAA GTAAATGCTT CATAAAGTAT	240
TCTTGACCTT TTGCAGAACT TGAAATTAAG	
TTTGAACGCC ATATAAATAA TGATTTTGGA	300
TGATTCTTTT CAAATCAGGA TCTTCTATTG	
CAAATTGTGG TTTGTnTTGG ATTTCACTn	360
TC ATCAATTGCA CGTTGCAAAA TCGCTTCATG	
TGAATCTATA CCCTGCATCT TGTAGCnTCC	390

(2) INFORMATION FOR SEQ ID NO: 4031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4031:

TGGTTCGAAT CCAGCTAGCC CAGTTATTGG	60
CGGCATAGCA AGTGGTAAGG CAGAGGTCTG	
CAAAACCTTT ATCACC	120
GGTT CAAATCCGGT TGCCGCCTCC	
AGGTTTATGCGGGAGTAGTT	
CAACTTTTAG AACACGTTCC TTCCCGGAAn	180
GAGGTATAGG TGCAAATCCT ATCTTCCGCT	
CCATAATTTA ATAATAATGC GGGAGTATTT	240
CAACTCTTAG AATACATTCC TTCCTGGAAT	
GAGGTATAGG TGTAATCCT ATCTTCCGCT	300
CCATAATTTA ATATTTGCGG GGAGTAGTTC	
CAACTTTTAG AACACGTTCC TTCCCGGGAA	360
GGAGGTATAn GTGTATCCTA TCTTCCGCn	
CATAATGCCT TCCAAAGGGG AATTTTTTTGG	400
TTTnACCATT	

(2) INFORMATION FOR SEQ ID NO: 4032:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4032:

```
GTATCGATGA GTTTCTTCGG TCGTCTTCG ACAGCCATTT TGACTTCGAC AAAATGCATC      60
ACATCGGGAT GACCATTAAT TGCATTAAC GTGTCTTGTA AATCTTTTGA TGATTCAACG      120
TCATGAATTT CAACATTTTT ACCACCAAAT ACAGCTGGTA AAGCTTTATA ATCCCACATG      180
TGAATTTTCA TATAAGGTTT ATACATGCCG TGAATAAGTC GTTCTACCGT rTrGCCGTCA      240
TTATTAATCA CCAATAATAC CGGGTTAATA TGCTGTCTAA TCATAGTTGG AATAGCTTG      300
AACAGTTAGT TGGCCATGAG CCATCACCCA TTTAATAATA AGTTACGACG GATCTTTGGT      360
CTGCCAATTG GGGGAnCnCA ATGTTGCAGG GnAATGGTAT      400
```

(2) INFORMATION FOR SEQ ID NO: 4033:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4033:

```
CACGACGTTC TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTgGG      60
ACCGACTACA GCCCCcAGGA TGCGATGAGC CGACATCGAG GTGCCAAACt CCCCgTCGAT      120
GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCgGGGTA GCTTTTATCC GTTGAGCGAT      180
GGCCCTTCCA TGCgGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT      240
AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTCC AACCATtCTG      300
AGGGAACTTT GAAGCGCTCC GTACCTTTTA AGAnGGCGAC CGGCCcAGTC AAActGGCCG      360
CTGACACTGT CTTCCAACAC GATAAGTGGT GCGGGTTAGA      400
```

(2) INFORMATION FOR SEQ ID NO: 4034:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4034:

AATTCCATGT GTACGGTTGA AATGCGCAGA GATATGGAGG AACACCAEG nCGAAGCGAC	60
TTTCTGGTCT GTAAGTGACG CTGATGTGCG AAACGTGGGG ATCAAACAGG ATTAGATACC	120
CTGGTAGTCC ACGCCGTAAA CGATGAGTGC TAAGTGTTAG GGGGTTTCCG CCCCTTAGTG	180
CTGCAGCTAA CGCATTAAAGC ACTCCGCCTG GGGAGTACGA CCGCAAGTTG GAAACTCAAA	240
GGAATTGACG GGGACCCGCA CAAGCGTGn AGCATGTGGT TTAnTTCGAA CAACGCAGAG	300
AACCTTACCA AATCTTGACA TCCTTTGACA ACTCTAGAGA TAAAGCCTCC CCTTCGGGA	360
CAAATGACAG TGGTGCAngT TGTCTCACT CGTGTCGTGA	400

(2) INFORMATION FOR SEQ ID NO: 4035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4035:

TTCGCTTTGC CCGTCTGTCA CATACTGTA AAATTCTATA AATAGAATTT TTGATGACGG	60
GTCCCTTCCT AGGGTGCCGT CTCAGCCACC CCAACCGGCA CATTGTTGTA AGCTGACTAT	120
ATGTCACTTC TGTGTTGGGG CCCCTGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC	180
CATTAATACT ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACATTAAAGCCCAAATTAAT	240
CAAAAGCTTT CTGAACCAGA AACGAAAAAA ATCTATAGTC ATAGAAAAAT TTATGTAGAG	300
CCTGTTTTTTG GATTTATGAA GGCTATTTGG GGTTCACG AATGTCAGTT CGAGGAATAA	360
TnAAGTnAAC GAGAGCCAGG TTTGTAATTA TGGCACTnAT	400

(2) INFORMATION FOR SEQ ID NO: 4036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4036:

TAAATGTTGA AAAAGCACGA TTAGATAGAA TTTTGAATAA CAATGAAATT CGTCAAATGA	60
TCACAGCATT TGGTACAGGA ATCGGTGGCG ACTTTGATCT AGCGAAAGCA AGATATCACA	120
AAATCGTCAT TATGACTGAT GCCGATGTGG ATGGAGCGCA TATTAGAACA TTGTTATTAA	180

CATTCTTCTA TCGATTTATG AGACCTTAA TTGAAGCAGG CTATGTGTAT ATTGCACAGC	240
CACCGTTGTA TAAACTGACA CAAGGTAAAC AAAAGTATTA TGTATACAAT GATAGGGGAC	300
TTGATAAACT TAAATCTGAA TTGAATCCAA CACCAAATG GCTATTGCAC GTACAAAGGC	360
TTGGAGAATG AATGCAGTCC ATTTGGGAAC ACATGACCTG	400

(2) INFORMATION FOR SEQ ID NO: 4037:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4037:

TCGTCGCTAA AGACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT CTCCTTCGGC	60
TCTCGCTTAC TCATTTAGCT CTAATAAACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT	120
CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT	180
AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA TTTTTTGCCT	240
GGCAACGTTT TACTCTAGCG GAAnTAAATT GGGCTACCAT CGACGCTAAG AACCTTTCTT	300
GACTTGTGAC AATCGCTTGC TTCTTTCCTC TTCTTCGGCT CTCGCTTACn CATTTAGCTC	360
TACnAAACTC GTTGCCTCT T	381

(2) INFORMATION FOR SEQ ID NO: 4038:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4038:

CTGTTTGTCA TACTTCATAA ATCCTTTAAA TTCACCCATC GTATCTCCCC CTTTCCTTAA	60
TACACAACGG CTGGTTTATG TTTAGCATCG ATTGTTTAC TGTCATCGTA AAATGCAGCT	120
AACATCGCTT CATCTTCATT GTCATGTAAT GATTTGTGCA AATGAATTT TTGCATCATT	180
AATTGATAAT CTTTAGGAAT AACTTTAACG ACGACATCTT CAATGCGATC AAAATGTTTT	240
AACACATGAA TCGCTCTCGT ACTATTCGTG TGTGACACAT GTnCTTCCAG CATTTGCTTA	300
ATGAATGCTT TTnCTTCTTG GTGTTTAATC TTTGTAAACG AAAGCGTATC TAGTGATAnG	360

(2) INFORMATION FOR SEQ ID NO: 4039:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4039:

```

AGTGCGAACC CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC      60
GCATATGTTT TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAG TGAnTGCACT      120
CACCGCAGAT TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG      180
GAGCAGAAGA CGGGATTCTGA ACCGCGACC CCAACCTTGG CAAGGTTGTA TTCTACCGCT      240
GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GCTnAGGATC      300
CTAAGTCTAG TGCCTCTGCC AATTCCGCCA CACCCGCAA TGGTGAGCCA TAGAGGATTC      360
GAACCTCTGG ACCCTCTGGA TTAAAAAGTC AGATGCTCTA      400

```

(2) INFORMATION FOR SEQ ID NO: 4040:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4040:

```

CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT      60
TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT      120
TCGCCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAG      180
AGACCTCACG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA      240
CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC      300
GGCTCTCGCn TACTCATTTA GCTCnACTAA ACTCGTTGCG CTCTTGTCT CGTTTCGGGC      360
AGATTCAAAC GnTTGTCA      378

```

(2) INFORMATION FOR SEQ ID NO: 4041:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4041:

GTACCTTAAC AATATCTCGA AATGGACGAA CTAAATTATG AACCGCATGA AAGGATACTT	60
GCGAATCATT TGAGCATGCT TGAATCATAA TATCACCATC GCTGTAATCG TCTATTAACT	120
GATCATTCGG AAAATGCGGT AAATCTTTAA AGGCATCGGG AATTTCTA GATAACCCAA	180
TTTTCTTCAT CAAAGACTTA CTAATCCCAA AGGTAATCGT TAACTTGCTT GCACCTAATC	240
CTATCGATTC ACCGGTATCT ACTGGTGGGC ATTAAAGGAT TGTTACTCGG GCTTGGCCAA	300
CTGTATCACC ATCCATCATA CGATTCAGCC ATAACGGTCC ACTTTTTTAA ACATTGGCTT	360
TATTGGCACC CnAACCTTTG GACTTCnAAT CTAACGGCCA	400

(2) INFORMATION FOR SEQ ID NO: 4042:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4042:

GACTTGCAAA CGTTGTGATG ACGGTCAAGA AACTGGTAA CACACCAGAC GGACGTAAAG	60
CTGGCGAACC ATTTGCTCCA GGTGCAAACC CAATGCATGG CCGTGACCAA AAAGGTGCAT	120
TATCTTCATT AAGTTCTGTA GCTAAGATCC CTTACGATTG CTGTAAAGAT GGTATTTCAA	180
ATACATTCAG TATCGTACCA AAATCATTAG GTAAAGAACC AGAAGATCAA AACCGTAACT	240
TAACTAGTAT GTTAGATGGT TACGCAATGC AATGTGGTCA CCACTTAAAT ATTAACGTAT	300
TTAACCGTGA AACATTAATA GATGCAATGG AACATCCAGA AGGAATAEC ACAGTTAACA	360
ATCCGTGTAT CTGGTTACGC TGTTAACTTC ATTAAATTAA	400

(2) INFORMATION FOR SEQ ID NO: 4043:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4043:

CTATTTTATC TAAAGTTAAA CCTGACCCAC CTAGAATTGA CGCAAACCTCT GTGACATATA	60
AAGCAGGTCT TACAAACCAA GAnATTAAAG TTAATAACGT ATTAAATAAC TCGTCAGTAA	120
AATTATTTAA AGCAGATAAT ACACCATTAA ATGTCACAAA TATTACTCAT GGTAGCGGTT	180
TTAGTTCGGT TGTGACAGTA AGTGACGCGT TACCAAATGG CGGAATTAAA GCAAATCTT	240
CAATTTCAAT GAACAATGTG ACGTATACGA CGCAAGACGA ACATGGTCAA GTTGTTACAG	300

TAACAAGAAA TGAATCTGTT GATTCAAATG ACAGTGCACA GTGAACAGTG GACACCACAA 360
 TTGACAAGCC AACTACTGAA GGCGCnGTGn TTATTAAAAG 400

(2) INFORMATION FOR SEQ ID NO: 4044:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4044:

AAAATGGCTT GATTTGAAAA ACGACCAGCA TCGCTACTG GnATAATAGC GAGGCTACCA 60
 TGTGTGTTTCA TCGTAGnCGC ATGTTAGTTA ATCCAGGGAT ACAECATCA TGATCAATAT 120
 TAAAGCCATA TTCAAACAAT TGACCATAAG GTTCAATGTA AGCAGCGCCG GTGCACTTGC 180
 ATTCCAGCTG AATTAGAGCG ACGTGCAGCA TAAGCCAAGT CTTCTTTTGT AATATAGCCT 240
 TCTTTTGTGTTG ATGTGTTTAC GGTCCATTGG GTGGATAATA CAAAGCGATT CGAAATTTTG 300
 ATGCCATTAG GTAAGTGGAT TGATTGTAAA AGTGGTTTGT ATCGGTACAT ACTATGATTC 360
 CnTTTCCATT GCAAT 375

(2) INFORMATION FOR SEQ ID NO: 4045:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4045:

GTTCCAATGA AGATAGCTAG AAATGATATC CAAAACACAT GATGCATCAC TGGTGATGCT 60
 CGACTAATTG TATTCCATGA TGCATTAATA ATAATGACCA ATACACATAA AATAAGCAGC 120
 CATTTATCGT TTATTTTAAA AATATAATGC AGCAAAAATC CCAAAATGAT TAATTGCACA 180
 ACTGCTCGTA ATGTCGCAAC AATTAAATCT TTAATAATAT GTAAACCTTC TTTATATGAA 240
 ATGATAATCG GAATGACTAA AAGCAATGCC GTCAATCCAA GTGCCCAT ACTCATGTnG 300
 ATTCAACTCC TCTGTATTAG AAATTTGACC ATCAACAATT GTTATACGCT TTTTGnAAGT 360
 GGTCGCATAC TTTGGGGCAT CGCTGTGGGG TAGGGGGnCn 400

(2) INFORMATION FOR SEQ ID NO: 4046:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4046:

CGAGTCTGAG TCGCTGTCTG AATCTGAATC GCTGTCTGAG TCCGAATCGC TATCTGAATC	60
TGAGTCGCTG TCTGAGTCTG AATCGCTATC TGAATCTGAG TCGCTATCTG AGTCTGAGTC	120
GCTGTCTGAG TCTGAGTCGC TGTCTGAGTC TGAATCGCTA TCTGAATCTG AGTCGCTGTC	180
TGAGTCTGAG TCGCTATCTG AGTCTGAGTC GCTGTCTGAA TCTGGAGTCG CTGTCTGAAT	240
CTGGAATCGC TGTCTGGAGT CTAATCGCT ATCTGAGTCT GGAATCGCTA TCTGAGTCTG	300
AATCACTGGT CTGGAGTCCG AGTCACTGTC TGAATCTGAC TGCACTnACn GGATTCTGAG	360
TCGCTAACnG GAATC	375

(2) INFORMATION FOR SEQ ID NO: 4047:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4047:

ATGGGTAAAA AGGCATTAGA GTCAATCATT GATAACGCTG AAAAAACAAC TCAAGAGCGT	60
TTACGTTTACG GATATGAAGA TGCTGTAGAT TATAACCGTT ATGTCGGTAA TATTTATACT	120
GGATCATTAT ATTTAAGCCT AATATCATT CTTGAAAATC GAGATTTACA AGCTGGTGAA	180
ACAATCGGTT TATTCAGTTA TGGCTCAGGT TCAGTTGGTG AATTTTATAG TGCGACATTA	240
GTTGAAGGCT ACAAAGATCA TTTAGATCAA GCTGCACATA AAGCATTATT AAATAACCGT	300
ACTGAnGTAT CTGTTGGATG GCATATGGAA ACATTCTTCC AAACGTTTTG GATGACGGTG	360
GAATTTGACG GnGGACCAAG ATGChTGTTC CAGGAGGTCC	400

(2) INFORMATION FOR SEQ ID NO: 4048:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4048:

CAAACCATCT GACATAATAT AACTTGGAT GTTAGATAAG GGTTTGCCAA TTGGAATCGT	60
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CTCAGGTATC AATCACCACA ATGATGTGAC CAATACGATG TGATGACTGT TGA	120
CTCAGGTATC AATCACCACA ATGATGTGAC CAATACGATG TGATGACTGT TGA	
GGTCCATAGG CATTGAAATA CGTGCCACAA TGCTTCTCAA TATATTTAAC AAAGGATGCC	180
GGTCCATAGG CATTGAAATA CGTGCCACAA TGCTTCTCAA TATATTTAAC AAAGGATGCC	
GTACTAGTTG CCCCGCCTGT AATCAACTTT TCAATATAAA AGTCTCCAT AACACTACAC	240
GTACTAGTTG CCCCGCCTGT AATCAACTTT TCAATATAAA AGTCTCCAT AACACTACAC	
ATCTGTAACG GAATCGACGC AACCGTCACA CGATGCTTAT TAATGAGTTG TTGTA	300
ATCTGTAACG GAATCGACGC AACCGTCACA CGATGCTTAT TAATGAGTTG TTGTA	
TCTGGATTAA CACGnTCCTC TCTATCTGGA nTCACAAGCG TATGACCATT AACAAACAAC	360
TCTGGATTAA CACGnTCCTC TCTATCTGGA nTCACAAGCG TATGACCATT AACAAACAAC	
AATAAATCTC CATAACTGnT GCATCAAAAA CATATTGCAT	400

(2) INFORMATION FOR SEQ ID NO: 4049:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4049:

TCTGCATGTT CTCGAGATCC ACCAAATGTT AAATGGGTAT GTGCATCTAC TAATGCTGGG	60
TCTGCATGTT CTCGAGATCC ACCAAATGTT AAATGGGTAT GTGCATCTAC TAATGCTGGG	
GACACTACCT TCCCCTAGC ATCAATCGTC TCAGTCGCAT CGTAGTCATC TGTATGTGTT	120
GACACTACCT TCCCCTAGC ATCAATCGTC TCAGTCGCAT CGTAGTCATC TGTATGTGTT	
CCAGCATATA CAATTTTGGC CATCTTTAAT GACAACTGTA CCATTTTTC CAACATTTGA	180
CCAGCATATA CAATTTTGGC CATCTTTAAT GACAACTGTA CCATTTTTC CAACATTTGA	
ATTCATCTAA TTCCTTACCC TTCAAAGGTT TATCTGTTGA TCTCGGTAAA ATTAATTGCT	240
ATTCATCTAA TTCCTTACCC TTCAAAGGTT TATCTGTTGA TCTCGGTAAA ATTAATTGCT	
GCTATATGAT TAnTATTAAA TCATTCATTA CTATCACCTG CTTATCAATC ATGGAATAGA	300
GCTATATGAT TAnTATTAAA TCATTCATTA CTATCACCTG CTTATCAATC ATGGAATAGA	
ATACCTTTTC nTTAGCGTTT GAATAGCGAG TCATAGCCAG CATCAACATG TCGGGCAACA	360
ATACCTTTTC nTTAGCGTTT GAATAGCGAG TCATAGCCAG CATCAACATG TCGGGCAACA	
CCCATACCGG GGTCATCGTC CAATACACGT TCCAAAnCTnC	400

(2) INFORMATION FOR SEQ ID NO: 4050:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4050:

ATCACCCATG TTCTGACTCC CAAGTTAAAT TAATTGGCAT TCGGAGTTTG TCTGAATT	60
ATCACCCATG TTCTGACTCC CAAGTTAAAT TAATTGGCAT TCGGAGTTTG TCTGAATT	
GTAACCCGAG AGGGGCCCCCT CGTCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG	120
GTAACCCGAG AGGGGCCCCCT CGTCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG	
GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTTCGATT GGAATTTCTC	180
GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTTCGATT GGAATTTCTC	
CGCTACCCTC AGTTCATCCG CTCACCTTTT AACGTAAGTC GGTTCGGTCC TCCATT	240
CGCTACCCTC AGTTCATCCG CTCACCTTTT AACGTAAGTC GGTTCGGTCC TCCATT	
GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACAAATA	300

CTAAACGCCT ATTCAGCTCG nTTCGTACGG CTCCACATTT ACTGCTAA_nC TTGCATCAAT 360
 CGTACTCGCG GTCAATCTAC AAAG_nACGC ATCACCAnTA 400

(2) INFORMATION FOR SEQ ID NO: 4051:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4051:

AGTGAAAATG ACTTTATCGG GCTGTTTCAGC GATATGGATT TGAGTTCAAC GCGACTAGGT 60
 AACAAATGTCA AAGAACGTAC TGCTTTAATC TCTAAAGTCA TGGTTAATCT TGACGACTTA 120
 CCATTCGTTC ACAGTGACAT GGAAATTGAT ATGTTAGGTG AECATATGA ATTCCTAATC 180
 GGGCGCTTTG CGGCGACAGC GGGTAAAAAA GCAGGCGAGT TCTATACACC ACAACAAGTA 240
 TCTAAGATAC TGGCGAAGTT GTCACAGACG GTAAAGAT_nA ATTACGTCAC GTGTAACGAC 300
 CCAACATGTG GGnTCCGGTT CATTGTGGTA ACGTGTTGGT AAAGAACGCA AGTGTATCGT 360
 TAATTCGGAC nAAGAACGTA ACAATACTAC nTACGACTTA 400

(2) INFORMATION FOR SEQ ID NO: 4052:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4052:

TCCTACAACC CCAACAAGCA AGCTTGTGGT GTTGGGCTCT TCCCGTTTCG CTCGCCGCTA 60
 CTAAGGGAAT CGAATTTTCT TTCTCTTCCT CCGGGTACTA AGATGTTTCA GTTCTCCGGG 120
 TGTGCCTTCT GATATGCTAT GTATTCACAT ATCGATAACA TGACATAACT CATGCTGGGT 180
 TTCCCCATTC GGAAATCTCT GGATCAAAGC TTA_nCTTACAG CTCCCCAAAG CATATCGTCG 240
 TTAGTAACGT CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGGC CCTTAATAAC 300
 TTAATC_nATG TTTTCCACCA TTTTTTATAA GT_nCAAAGGC TTCA_nATACG GCTTCGGTTT 360
 TTCATTAATT TTAAATGGC_n CAATTTAACA 390

(2) INFORMATION FOR SEQ ID NO: 4053:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4053:

```
AACATACCGA TGTATATAAT CTATACACAA AGGATAATTA CTTATGCAA GCGGAGGAA      60
TCACATGTCT ATTACTGAAA AACAACGTCA GCAACAAGCT GAATTACATA AAAAATTATG    120
GTCGATTGCG AATGATTTAA GAGGGAACAT GGATGCGAGT GAATTCCGTA ATTACATTTT    180
AGGCTTGATT TTCTATCGCT TCTTATCTGA AAAAGCCGAA CAAGAATATG CAGATGCCTT    240
GTCAGGTGAA GACATCACGT ATCAAGAAGC ATGGGCAGAT GAAGAATATC GTGAAGACTT    300
AAAAGCAGAA TTAATTGATC AAAGTCGGTT ACTTCATTGA GCCACAAGAT TTATTCAGTG    360
CGATGATCGT GAAATTGAnA CGCAnGATTT CCGATATAGA      400
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(2) INFORMATION FOR SEQ ID NO: 4054:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4054:

```
GTAAGACCAT CGTACTTGAG TCTTCAAGTG TTCTTGATAA AACGGAACGA GAGACTTGGT      60
ATTTTTCGAA CAAATCTTTC ATTAACACAC CGACCATAATAATTACAATC GAAGCAACAC    120
CTGCAGCGAA TACAAGCGCA ATACAACAAA TAACAGTAAT ACATATTAAA CTTCTACAG      180
AATGGATGCC TTTAGAAATA GTAGTTAATA AGACTTCTAA ACATCCTGCT TTTTCTACAA    240
TACCTGCAA TGCATATCCG CAAAATATCG TTAATAATAT TTGGGnCAT CTCATCATAC      300
CACCCTGTTC TAACAAGCTT TCACACTGGA TGAATATGAG nTGATGTATC ATTGATCGTT    360
AAACCCTAAT GTGCTTTGAA CCATCGTCAT TTGAATGTGA      400
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(2) INFORMATION FOR SEQ ID NO: 4055:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4055:

```
CGTCTACAAG TTCAAAATTC AAGTCTTCCA TAATTGGTTT AACAATCACT TCTACTTGTT      60
```

CTGTAATTTT ACTCATACAG GCCTCCCTTT TTGGCAAATA GAAAAGAGCG GGAATCTCCC	120
ACTCTTCTGC CTGAGTTCAC TAATTTTAA GCAACTTAAT TATAGCATAA GTTTATGCTT	180
GAAACAAATG ACTTCACTAT TAATCAGAGA TTCTTGTAAG AGTTTGTTCC TTTATTTTAC	240
CATTACATTT GAATAGACTC GTAAGACATT GAAAAGAAAT AGGGCATAA TTTTGTGTCC	300
AGCAGCAATT TTGTATTTCT TTGACTACGG CATACGGATT AAATAAATAC CTTGATTATT	360
TCATTTTACA TATCAAATAT CGGAAGTTGA GCTTTATCTG	400

(2) INFORMATION FOR SEQ ID NO: 4056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4056:

ATTTTGTTT ACTTCATGTT GAGTTTGTAGA CATTTTAACC ATCTCCAATA TAAAAATAAA	60
TTAAATTAATA TTCTCAGGGA CTTGCATGAC GCCACCTGTA TTTGCGCTAG TTAGTAGGGC	120
AGTATAACGA GCTAGATAAC CTGTTTTTAC TTTCGCTTTA AATGGTGTTA AAGATTCTCG	180
GCGACGCGCT AGAACATCTT CAGGCTGGTT TACGTTTAAT GTACGATTG TTAAATCAAT	240
AGTAATCTCA TCACCATCTT CAATTAAgGc AATTGGTCCA CCAGATGCAG CTCAGGGGA	300
AATATGaCCA ACTGcAATAC CTCTTGTTGGc ACCGGtAAAA ACGCCCATCA GTkaATTAAT	360
GCaACATCTT TACCTAAGCC GCGaCCAACA ATAGAGGAAG TAGGTGCTAA CATTTTCAGG	420
nCATACCTGG GTCCACCTTT TAGGTGCCCTT TCAnTATCTn ATGACAACG ACGTGGGCCT	480
G	481

(2) INFORMATION FOR SEQ ID NO: 4057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4057:

TTTTTGCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT GGCTACCATC GTCGCTAAAG	60
ACCTTTCTTG ACTTGAGACA ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC	120
ATTTAGCTCT ACTAACTCG TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA	180
CTTCGCCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GGACGTTTTA GACATAAAAA	240

AAAGAGACCT TCGGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT	300
ACTCTAGCGG AAGTAAATTG GGCTACCA _n C GACGCTAAGA ACCTTTCTTG GACTGTGACA	360
ATCGGCTG _{Cn} TCTGT _n CCT	379

(2) INFORMATION FOR SEQ ID NO: 4058:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4058:

CTGCATCACT GCCATAAAAA CTACCGTCAG CAGCGATAG _n CGGCCAATCA TACCAGGAAC	60
AAGACCGGGC TTGTCAGCGA TACTAACAGC GATATATCCAGCTAGTATTG GAACCATAAA	120
TTTAAAGGCT AAAC _T ACCAA TGTTTTCAAT GGATTTCCAA AATGAATCAT CTGGGATGAC	180
TAATCCTTTT GATGTCGTTT CACCGCCTAG AGTCAGCGCG ATGGCGATAA GGAGTCCACC	240
AACTACGATA AAAGGAACCA TAAACGATAC ACCGTTTATT AAATGTTGAT ACACCATTTG	300
AATACCATTT TAGACT _n ACC GCGATCTTTC GAATGATAAT TTGTTTCAGA TGGTTAAATA	360
GGCGCATTTG ATTTAATGAT ACGTGGATTT GGACCCTCGG	400

(2) INFORMATION FOR SEQ ID NO: 4059:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4059:

TTAAAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAACTA AGT _n GAnCTA CCATCGACGC	60
TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC	120
CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT	180
TCGCAAAACA TTTATTTTGG ATTAAGTCTT CGATCGATTA GTATTCGTCA GCTCCACATG	240
TCACCATGCT TCCACCTCGG AACCTATTAA CCTCATCATC TTGGAGGGA TCTTATAAAC	300
CGAAATTGGG GAAATCTCAT CTTGAGGGGG GCTT _n CATGC TTAGATGCTT TCCAGCACTT	360
ATCCCGT	367

(2) INFORMATION FOR SEQ ID NO: 4060:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4060:

TTCCGnACTC ACATAGCGAC TCAGGATTCA GACAGCGCAT TCAGATTCAG ACACCGCATT	60
CAGATTCAGC ATAGCGATTG AGCATTCCGC ACAGTGACTC AGnATTCCGA CAGTGACTCG	120
GATTCAGATA GCGATTGAGA TTCCGACAGT GACTCAGATT CCGACAGTGA CTCAGACTCA	180
GACAGTGATT CGGATTGAGC GAGTGATTGCG GATTCAGATA GTGATTCCGA CTCCGACAGT	240
GACTCGGATT CAGATAGCGA CTCAGACTCG GATAGCGACT CGGATTGAGA TAGCGATTGCG	300
GACTCAGATA GCGATTGAGA ATCAGACAGC GATTCAGATT CAGACAGCGA CTCAGACAGT	360
GACTCAGATT CAGA	374

(2) INFORMATION FOR SEQ ID NO: 4061:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4061:

AAAATCATAA TATTTGGCAA TTTTTTCAAC TTGACTCTG TCCTTCTGCA TAACTGCCGT	60
AAATAATTCA CCTTCATCAC ACGCTGTACC TACCAATAAT CCCTCACGAT ATTCATCTAA	120
CAATGAACGT GGAATTCGAG GTGTACGGTA GAAATACTTC ACCAATGATG CACTTACAAT	180
TTTAAATAGA TTTTAAAGAC CTTGTTGGTT TTGTACAATT AATGTGACAT GACTAGGTCT	240
TGCACGTTTA TATGCATCTT CATTACTGAG TTTTtkGtG ATTTGTTAT GATTTAATAC	300
GCCTAAwTCy TTCATTTGTT GAACCATTTT TATGAAAATG TAAGCTGTTG CTTCTGTATC	360
ATAAATGGCA CGGTGATGTT GCGTTAATTC TACGCCATAT TTTTtagCCA AGAAATTCAA	420
ACCATGTTTA CC	432

(2) INFORMATION FOR SEQ ID NO: 4062:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4062:

TATCTTCGTT CTCAATAGAA TGATTTAAAC CTTCGATTTC TTTATCTAAA TGACTACCAA	60
TTAAATCTAT TTCTTCTATT GTTAAATCGC TATCTCCATC TTCTTTTATC TCTGGTATTA	120
TTTTTTCTTC AACTAAGTCA CGATATAATG TTTTGAATTTTCGTTCAAT TTCGATTTCGT	180
GATTTTGAAT ACTTTTCTTC CACACAAATG TATACCTATT GGCATTAGCT TCTACTTTTG	240
TACCATCAAT AAGATTTTGC TTAAACATT GACTATGAAA CTGGGATAAA TAAAGAnTCA	300
ATTAACGCAT CAGTATTAGG GAnTCACTCT AATACGATTA ATAGTTTTTA TAAGAAGGTG	360
nTTGGATTTG GAGCTAACCA CATCCA	386

(2) INFORMATION FOR SEQ ID NO: 4063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4063:

TAGGAGAGCG TTCTAAGGGC GTAGCATGAT CGTAAGGACA TGTGGAGCGC TTAGGAGAAT	60
GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT AAGGTTTCCA	120
GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCCTAAGC TGAGGCCGAC ACGTAGGGCG	180
ATGGATAACA GGTTGATATT CCTGTACCAC CTATGAATCG TTTTAATCGA TGGGGGGACG	240
CATAGGTATA GGCGAGGTGA CGATTGGGAT TGCACGTCTT AAGCAGTAAG GCTGAGTATT	300
AGGCAAATCC GGTACTCGTT nAAGGCTTGA GCTGTGGATG GGAGAAGAC ATnAGTCTT	360
CGAGTTCGTT GGnTTTCACA ATGGCC	386

(2) INFORMATION FOR SEQ ID NO: 4064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4064:

TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTC	60
TACTCTAGCG GAACGTAAGT TGGAGCTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT	120
CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT	180

ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA	240
AGTCTTCGAT CGAnTAGTAT TCGTCAGCTC CACATGTCAC CATGCTTCCA CCTCGAACCT	300
ATTAACCTCA TCATCTTTG GGGGATCTTA TAACCGAAGT TGGGGAAATC TTCAhCTTGn	360
AGGGGGGGCT TCATGCCTTT AGAATG	386

(2) INFORMATION FOR SEQ ID NO: 4065:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4065:

AATTCTTTTCG CTACTTGAAT GACAACACTT TGTTTTACGC CTGAAATGGC TTCTTGCCAA	60
GCAGGTGTAT ATTTTGATTC TGCATCGTCG TATCCTTTT ATTCTAATTT ATGATCAAAA	120
CGACGCACGC CATATTGACT TGCCATTAAG TCAAAAATTG TAGCAATACG GACTTTGTCA	180
CCATTTGCTA AAGTGACTTG TCGAGTTGGA ATTGGACGAT TGAATATCCC ATCTCCATCA	240
CTATCAAAGT ATGGGAATTG AATTGTTTCT AATTCGTATC CACCTTCTGT CATTGATAAT	300
GTAGGGTTAA TTTTAGAACC ATCTTCTGTT TCTAGTTTTA AGTTCCACTT CTTACCTTCT	360
TCCCAACGTG GACCCATGGT GCCATTAnGn ACTACTAAAC	400

(2) INFORMATION FOR SEQ ID NO: 4066:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4066:

ATTTTGAAAT TGAGAAAACA ACTTATTGAA AAACATAATC TTTACGGTAA CATGGGTTCa	60
GGAACAATCG TTATTAAAAT GAAAACGGT GGGAAATATA CGTTTGAATT ACACAAAAAA	120
CTGCAGAGCA TCGTATGGCA GACGTCATAG ATGGCACTAA TATTGATAAC ATTGAAGTGA	180
ATATAAAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA TCGGAAAAAC AAGAAGTTAA	240
GTGACAACGG TTTACATGTT GCTTAGCTTC TTTTATTATGCGTAATGATG TAAAAAGACG	300
nATATTTCATT TGTTTGTAAG AGTGGCATTC TATGTCTTAA AGTGACGnAA CTTCCAATGT	360
GCCCAGTGTT TGATTCACAT CAAATCCATT TTTATTTAAC	400

(2) INFORMATION FOR SEQ ID NO: 4067:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4067:

CCTCATTCCA GGAAGGAATG TATTCTAAGA GTTGAAATAC TCCCGCATT	60
TTATTAAATT ATGGAGCGGA AGATAGGATT TGCACCTATA CCTCGTTCCG	120
GGAAGGAACG TGTTCTAAAA GTTGAACTAC TCCCGCATAA	180
ACCTGGAGGC GGCAACCGGA TTTGAACCGG TGATAAAGGT	240
TTTGCAGACC TCTGCCTTAC CACTTGGCTA TGCCGCCAAT	300
AACTGGGCTA GCTGGATTCTG AACCAACGAG TGACGGAGTC	360
AAAGTCCGTT GCCTTACCGC TTGGCTATAG CCCATTAATA	400
ATAAGGGCGG CTGAAGGGGA TCGAACCCTC GAATGTCGGA	
ACCACAATCC GATGTGTAA CCACTTCACC ACAGCCGCCA	
TGGCAGGGGC AGTAGGAATC	

(2) INFORMATION FOR SEQ ID NO: 4068:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4068:

TATCTAATAG TTTTACTTTA AGTCCAGCAT TCACAAAG	60
TGCTGCCAGT TGAGCGCCCA TTGTGCCTGC	120
GCCAAGAACG GTTACTTTAT TAATTGTCAT AGTGATTCCT	180
CCAATTTAGT TGAGGATAAG ATAACCATTA AGATAATTGG	240
AATAACGTTG CTATTTTATA AAATTAATTA AGTATCTTTG	300
ACAGTCATCT TAGCCTCTTA TTTAAGGAAA AAGCTTTATG	360
CTTAAATAA GTCTTTTTTA GTGAAATTAA TGCATCTCAT	400
ATAATTATTT GCTATTTATA CGAAAGCAGA ATCTCCAGTC	
AAAGCGCGTC CAnTACTAAG GCATTAATTT CATGTGTACC	
TCGTACGTGT AAATCGnTTC TGCATCAGnG	
AGGAAACGTG CAATATCATA	

(2) INFORMATION FOR SEQ ID NO: 4069:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4069:

CAAAGGACCA ATTGCATTTG AGTATACACA TATTAATAAC AATACCGAAC GTGGTTGGTT	60
AAAAAGAAGA ATTGAAACGC CATATAAAGT AACGTTAAAT AATAACGAAA AAAGGGCACT	120
ATTCAAACAA TTAGCGTATG TTGAAGGGTT TGAAAAATAT CTTCATAAAA ACTTCGTTGG	180
TGCAAAGCGT TTTTCAATTC nCGGGGTTAGA CGCACTTGA CCGATGTTAC AACGTACTAT	240
TACGATTGCT GCGAAAGAAG GTATTAAAAA TATACAAATA GGCATGGCTC ACCGTGGGAC	300
GTTTAAACGT TTTTAACGCA TGTnCTTAGA AAAAACCGTA CGAAATGATG ATTTc	356

(2) INFORMATION FOR SEQ ID NO: 4070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4070:

AAACGTTTAG GGAAAATTAT CACACAGATA CAACAATACA CAGATATTGA TTACCCGAA	60
GCGATTGTCT TTCAAGCATC GTGTTTTAAC GAGTTTGTTG TTAAGGGGCG TTTAAGTAAT	120
ATTATTTCAA AATTGCAACA CTATTCAATT GAGGCGAAAC CAGGTATATG TATTATAGGG	180
GAAGTTGTTG ATTATACTGA AAACACTCCT AAATCATATG ATCCTATGAA GCAATTTTAT	240
GTAGTAAGTG GTTCTAAACA TGACGCCCTT ATGCTCTGTG AACATTATAT GACGAAGGTT	300
ATGGCTGTTG CTAAACCCCA ATGATACATC GAATGGGCAC CATTATCCAn TCGTCGCAAT	360
AATGGATTAC CCAAGGATGC CATTTAnTTA AGCCnGCCAn	400

(2) INFORMATION FOR SEQ ID NO: 4071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4071:

CCTCTGGAAA CCTTAGTCAA TCGGTGGACG GGATETCAC CCGTCTTTCG CTA CTCACAC	60
CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA CGCCCTTAGA	120
ACGCTCTCCT ACCATTGTCC AAAGGnATnC CCACAGCTTC GGTAATATGT TTAGCCCCGG	180
TACATTTTCG GCGCATGTGC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGGATGG	240
CTGCTTCTAA GCCAACATCC TAGTTGTCTG G GnAACGCCA CATCCTTTTC CACTTAACAT	300

ATATTTTGGG GACCTTGAGC TGGTGGTCTG GGGCTGTTTC GGGAACGGAA CACGGGACCT 360
T 361

(2) INFORMATION FOR SEQ ID NO: 4072:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4072:

ATGGTGACAA AAACATCGCA TTATTACTAG GTGTCGGCAC AGGCGTTTGT GGTGCTGCTG 60
CTATTGCCGC AGTCGCTCCA ATATTCAAAT CACGTGAAAA GGATACAGCT ATTAGTATCG 120
GTATCATCGC ATTGATTGGT ACGATATTTT CACTTATATA TACAGCTATC TACGCTATCT 180
TTTCAATGAC GACAAATGTT TATGGCGCTT GGTCTGGGT TAGTCTTCAT GAAATTGnCA 240
CACGTTGTCT TAGCTGGTGG CTTTGGTGGT AGTGATGCAC TTAAAATTGC ACTTCTTGGT 300
AAACTTGGTA GGAGTATTCT TACTGGATTC CCATTAACCA TCGTACTTAA TTTTAAATAT 360
GCGGTTnCCG TnCATCAGG AnTCATCTAG GCAAGGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 4073:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4073:

GCGACGATCA TTTTAGAATC CGCTTGGGCG ATTAATTCTT TAGAAGTGA TGAGGCAAAA 60
TGTTTCATTAT CAGGAACTAA AGCAGGTGCT GATATGAAAG ATGGTCTACG TATTCATGGT 120
GAAGACATGG GTACACTTTA TACCAAACAC GTTGAATTGG AAAACAAAGG CGTCGACTTT 180
TATGAAGGTA ATCAAGTGA TGAAGCTGAA GAAGAAGCAA AAGCTTGGAT TGATGCAGTT 240
GTAAATGATA CTGAACCAGT TGTGAACCGG AACAAGCAAT GGTAGTTACC AnAATTCTTG 300
AAGCGATTTA TCCGTCTGCC AAATCCAGGC CAAAGCCATT TACTTTGGAA TAACATCnTA 360
CCGGTAAGGG GGCnCATCCT GGACCAAATT TAAAAGTTG 400

(2) INFORMATION FOR SEQ ID NO: 4074:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4074:

TCTTCCTAAT ACCTTTCCAC GATCTTCAGC TGGCGCCTCT GCACTCGCAA ACGCACTTGA	60
TGCATCAACA ACACCACCAA ATAGTCCCTG CAATAACCTC ACAAGTACAA ACTGTAATGG	120
TGTCGTACAC AATGCCATTA AAAATAAGCA TACCGCCAAA CCAAGTAACG CTCTTAACA	180
CATCCATTTT CGGCTGATCT TATCACCTAG CTTCCCCCAT ATCGGCGGAG TTATGCATCG	240
TCGTTACAGC TGGAGCAGCA ATCGCTATAC CACTCCACAn CTGTATTTCT ACGGACTGAT	300
AGGATTTTGT AGTGATGnCC ATGATGAAAT GGGCAATAAT GGGCACAAAGT ACTGTTTCAGT	360
CCAGCCAATC GTTATGAAAC TGGACTGGGG CCATnAAATG	400

(2) INFORMATION FOR SEQ ID NO: 4075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4075:

GGTTCAGAAC GTCGTATGnA GTTCGnTCCC TATCCGTCGT GGGCGTAGGA AATTTGAGAG	60
GAGCTGTCTT TAGTACGAGA GGACCGGGAT GGACATACCT CTGGTGTACC AGTTGTCGTG	120
CCAACGCATA GCTGGGTAGC TATGTGTGGA CGGGnAAGT GCTGAAACTC TAAGCATGAA	180
GGCCCCCTCA AGATGAGATT TCCCAACTTC GGTtATAAGA TCCCTCAAAG ATGATGAGGT	240
TAATAGGTTT CGAGGTGGAA GCATGGTGAC AtnTGGAGCT GACGAATACT AATCGATCGA	300
AGACTTAATC AAAATAAATG TTTTGCGACA AATCCACTTT TACTTACTAT CTAGTTTGAA	360
TGATAAATTA CATCCATATG	380

(2) INFORMATION FOR SEQ ID NO: 4076:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4076:

CAACGACTCG AAGACACAAT GTCTTCTCCC CATCACAGCT CAGCCTTAAC GAGTACCGGA	60
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TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC	120
CTACTGCGTC CCCCATCGA TTAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA	180
TCCATCGCCT ACGCCTGTCG GCCTCAGCTT AGGACCCGAC TAACCCAGAG CGGACGAGCC	240
TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC AnCCGTCTTT CGCTACTCAC	300
AnCGGCATTC TCACTTCTAA GCGGTCCACA TGTCTTÆGA TCATGCTTnA AGGCCTTAGG	360
AAGGTTCCTA CCATGGTCAA	380

(2) INFORMATION FOR SEQ ID NO: 4077:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4077:

GCAGGTCTGA CTCTAGAGGA TnCCCACGCG CGCAAGATTT AAATCGAAGA AACCAGCAAC	60
AGATTCCTCA AAATAGCGCG GCGAACAACG AAACATCAAA TAGTGACCT GCAGCTGTA	120
ATGGTGTAGC ATCAACGCCA CCAAGTGCAC CAAGTGGCGA TACTGCACCA AATAATAATG	180
TTACGCAAAA TACCGCACCA AATAGTAATA ATGCGCCTGT ATCGACTACA CCACAAAGTA	240
CAAGGCGGGA AnAAAGATGG TCAAAGTTTT GTAGATATAA CAACAACACA AGTCAGCACA	300
GCTAACGAGA ACACACAAAA CATTACAGAT AAAGATGTTA AATCAATGGA AGCGGCATTA	360
ACGGGCTCTT	370

(2) INFORMATION FOR SEQ ID NO: 4078:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4078:

AAACATTTTA TCAAATGGCA GAAGGACATG TGCCAAGACC ACCAGCGATG GTTGAAACAT	60
TGACTTATAT TAAAGAGTTT ATGAACCAAG TT>CGCA TAGCTAGTAT GAAACGTGGT	120
GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGG AATTAGGGAT	180
CGGTACTTTA TATGAAGACG TGCTGCTTCC ATTAAATGAG TGATGCGATT TTGGCATGAA	240
GGTCACCTTA AATGTACATT GTTGTAATAA AATTGCCTAT nAAATTTTAA GCACATAAA	300

TAAGAGGGGC CAACCATTGT TAGAnATAAC AACGGTTGGC TCTTTAAntG T

351

(2) INFORMATION FOR SEQ ID NO: 4079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4079:

TTGAAGTAAC TAAATTAATA TTATGTTGTT CAATTAAAAG CTTCATACAA ACCTAATCTA	60
TTTGCACTCC ACCGCTAACA CCGAACACTT GTCCGGTTGT ATAAGTTGAT TCTTCTGACG	120
CTAATAGCAC ATAAGTTCCA CATAACTCAA CAGGTTGACC TGCACGACCT AAAGGTGTTT	180
TTTGACCAAA TGTTGGGATT TACTTTGAG GTTGTCCACC AGAAATTTGT AATGGTGACC	240
AGAATGGACC AGGCGCTACA CAGTTCACCT TAATTCCTTT TGGTCCTAAT TCTTCTGAAA	300
AACTTTTAGT TAATGAAATA ATTGCTGCCT TTTGAGGGG CATAATCCAT GAAGAATAnG	360
GCCAGGGAnT AAAACCCTGG ACnAAAGAAG CCGTGGAAT	400

(2) INFORMATION FOR SEQ ID NO: 4080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4080:

TCGTTGGACA CAATCTGAAA AATAAATAGA TATAAATTCG CGAGATATAT TCGTATTTAT	60
AGTAAAATTA AATAAAGAGA TTATATAACA CGAGGAGTAG TAAGTATGAA ATTTAGAAA	120
TATATAGATC AACTTTTATT GAAGCCTGAG TCAACACGTA CGCAAATCGA TCAAATCATC	180
GATGAAGCGA AACATTACAA TTTTAAATCT GTATGTGTGA ATCCAACACA TGTTAAATAT	240
GCAGCAGAGC GACTAGCTGA TTCAGAGGTG CTCGTTTGTA CGGTAATAGG ATTCCCATTA	300
GGTGCGTCGA CAACTGGCAA CGAAAGCATT TGAAACAGAA GATGCAATTC AAAATGGTGC	360
AGATGAATTG GACATGGTCA TCCACATCGG CGCATTAATA	400

(2) INFORMATION FOR SEQ ID NO: 4081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4081:

CGACTAGTGA GCTATTACGC ACTCTTTAAA TGATGGCTGC TTCTAAGCCA ACATCCTAGT	60
TGTCTGGGCA ACGCACATCC TTTTCCACTT A CATATATT TTGGGACCTT AGCTGGTGGT	120
CTGGGCTGTT TCCCTnChCG AACACGGACC TTATCACCCA TGTCTGACT CCCAAGTTAA	180
ATTAATTGGC ATTCGGAGTT TGTCTGAATT CGGTAACCCG AGAGGGACCC CTCGTACCAA	240
ACAGTGCTCT ACCTCCAATA ATCATCACTT GGAGGCTAGC CCTAAAGCTA TTTACGGA	300
GAACCAGCTA TCTCCAGGTT CGATTGGAAT TTCTCCGCnA CCCTCAGTTC ATCCGCTCA	359

(2) INFORMATION FOR SEQ ID NO: 4082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4082:

TTTGACATTT AGTGTAAGCG TnTTACAAAT AAAGCGTGTT GTTTTTGAAT TAAATGCATT	60
TCACATTAGT ATTCATATTA TTTTtaggag GAATTTATAT GACATTTGAA AAAGAAACGG	120
TCTTAAAAAC ATTATTTCTT GAAGATGTAC TTAGTATTGC TAAAGGTTTA ACAGACGGTG	180
AAGTCGAATT TTTACAACAA GTAGATTCAT TGGCTAGAAA GTAAGTACCG TGGAAAATAT	240
TAATCAACAT TGGATAGACG CTACTGTACC CGAGGACTAT TTTAAAGATC TGGGGAGAAT	300
TAAATTATTT TAACAATCCA TTA C TTTACA AG E ATCGTC CAAACGCCAA AnGGCCTAGT	360
CCA A CTATTT nCAGTTTTT	379

(2) INFORMATION FOR SEQ ID NO: 4083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic add
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4083:

TTGAAACAGC CAGAGGTGTT TTATACCCAG GTGTTTCAGA TATGTATGAT GCGAAACAAT	60
ATGTTAAGCC AGTnAATAAT TCTTGGTCGA CAAATGCGCA ACATATGAAT TTCAATTTG	120
TTGGAACATA TGGTCCTAAC AAAGATGTTG TAGGCATATC TACTCGTCTT ATTAGAGTGA	180

CATATGATAA TAGACAAACA GAAGATTTAA CTATTTTATC TAAAGTTAAA CCTGACCCAC	240
CTAGAATTGA CGCAAACCTCT GTGACATATA AAGCAGGTCT TACAAACCAA GAAATTAAAG	300
TTAATAACGT ATTAATTAAC TCGTCCGTGA AATTATTTAA GCCGATAATA CACCATTAAA	360
TGTnCAAT ATTACCCnGG GTAGCGGGTT TTAGTTCCGG	400

(2) INFORMATION FOR SEQ ID NO: 4084:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4084:

AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCnAGGCAT CCACCGTGCG	60
CCCTTAATAA CTTAATCTAT GTTTCATCC TACAGGAAAC GCGTTAGTAA TCTTGTGAGT	120
GTTCTTTCGA ACATAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC	180
ACTCGGTTTT GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAT	240
TTCTTTTTAG TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTAATGT	300
TAAATAAACA TTCAAACCTG AATACAATAT GTCACATTAT TCCGCCATCT nCTGAAGAAG	360
ATGTTnCCGA ATATnATCCT TAGAAAGGAG GTGGATCCCA	400

(2) INFORMATION FOR SEQ ID NO: 4085:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4085:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA	60
CCTCTGCGT GCAAAGCAGG CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA	120
TTAATGGTGG GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT	180
GAACCAGCTG GAGCTATAGG CCCATTAATT TGGAATGAAC AAACATTCAA AACTGGAATA	240
CAATATGTCA CGTTATTCCG CATCTTCTGG AAGAAGATGT TTCCGAATAn ATCCTTAnGA	300
AAGGAGGTGA TCCnGCCGCA CCTTCCGATG ACGGCTACCT TGGTTGACGA nTTGCACCCC	360
AAGCATTTGT TCCCACCTTC GACGGCTGAG CTCCTAAAAG	400

(2) INFORMATION FOR SEQ ID NO: 4086:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4086:

GTCATTGGAA ACTGGAGnAC TTGAGTGCAG AAGAGGAAAG TGGAATTCCA GTGTAGCGG	60
TGAAATGCGC AGAGATATGG AGGAACACCA GTGGCGAAGC GACTTTCTGG TCTGTAAGTG	120
ACGCTGATGT GCGAAACGTG GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT	180
AAACGATGAG TGCTAAGTGT TAGGGGGTTT CCGCCCCTTA GTGCTGCAGC TAACGCATTA	240
AGCACTCCGC CTGGGGAGTA CGACCGCAAG TTGnAACTC CAAAGGAATT GACGGGCGCA	300
CAAGCGTGGG AGCATGTGGT TTAATTCGAA CCAACGnATA GAACCTTACC AAATCTTGGA	360
C	361

(2) INFORMATION FOR SEQ ID NO: 4087:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4087:

GACCTTGCAG GACTCGAACC TGCGACCnA CGGTTATGAG CCGTTAGCTC TAACCAACTG	60
AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA	120
CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT	180
AGTTTGTAAA TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TGGTGCAA	240
GCAGnCGCTC TCCCAGCTGA GCTAAAGCCC CCATAAATAA TTACAGTATA TCGGGAAGAC	300
AGGATTCGAA CCTGCGACCC CTTTCCCAAA CCAAGTGCTT TTACCAAGTT GGTACTTCCn	360
GTATAATTTA ACGGGCCCGA TAGGAGTTCG GAACCCTTAA	400

(2) INFORMATION FOR SEQ ID NO: 4088:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4088:

AGCTATTATT TTTGACAGAT TCCATATCGT TCAACATTTA AATAGAGAAC TTAATAAGTA	60
TCGTGTACAA GTTATGAATG AATACCGTAA TAAAAAAGGA CCTGATTATA CAATTTTAA	120
GAATAACTGG AAAGTCCTAT TGATGGATAC TAGTAAAACC ATATTTAGTA AATACAGATG	180
GAATAAATCT TTTAAGGCTT ATAAACGCTC ATCTGACATT GTAGGAATTC ATGCTTTC	240
AAGACGATAT ACTACGACAC TCCTACGAAC TTGTCCCAAG GGATTACGGA AAAGGCCCTA	300
AGGGTTATGT TAATTGGCCC TAAATTTATT AAATGCGTTT GAAATTCAGT TAGTTAAAAA	360
GTCTGTGAGT GAnGGGTGTA TGGGAAAGTG GTTAAAATAT	400

(2) INFORMATION FOR SEQ ID NO: 4089:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4089:

ATCGTTTTAG ATAAGACGGG TACATTACAA ATGGTCGTCC AGTCGTGACA GATTATCATG	60
GTGACAATCA AACGCTACAA CTAATTGCTA CTGCTGAAAA AGATTCTGAA CACCCATTGG	120
CAGAAGCCAT TGTCAATTAT GCAAAAGAAA AGCAATTAAT ATTAAGTGAG ACAACAACAT	180
TTAAAGCAGT ACCTGGGCCA TGGTATTGAA GCAACGATTG GATCATCACC ATATATTGGT	240
TGGTAACCGT GAAATTAATG GCTGACAATG GATATTAGCT TGCCTAAGCA TATTTnnGGA	300
TGGATTTAAC ACATTATGAA CGAGATGGTA AACTGCTAG CTCATTGCTG TTGAATTATT	360
nCATAACGGT ATCA	374

(2) INFORMATION FOR SEQ ID NO: 4090:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4090:

AATTGAACGT CAAACTCTGT GACATATAAA GnCAGGTCTT ACAAACCAAG nAAATTAAAG	60
TTAATAACGT ATTAAATAAC TCGTCAGTAA AATTATTTAA AGCAGATAAT ACACCATTAA	120
ATGTCACAAA TATTACTCAT GGTAGCTGTT TTTGTTTCGGT TGTGACAGTA ATGACGCGT	180
TACCAAATGG CGGAGTTAAA GCAAATCTT CAATTTCAAT GAACAATGTG ACGTATACGA	240

CGCAAGACGA ACATGGTCAA GTTGTTACAG TAACAAGAAA TGAATCTGTT GATTCAAATG	300
ACAGTGCACC AGTAACAGTG ACACCACAnT TACAAGCAAC TACTGAAGGC GCTGTATTTA	360
TTAAGTT	367

(2) INFORMATION FOR SEQ ID NO: 4091:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4091:

TAATATTATA TTGCTAGTAG TTGACTGAAT GAAAATGCGC TTGCAACAAG CTTTTTTC	60
CTCTAGTCAG GGGCCCCAAC ACAGAGAATT TCGAAAAGAA ATTCTACAGG CAATGCGAGT	120
TGGGGTGTGG GCCCCAACAC AGAGAATTC GAAAAGAAAT TCTACAGGCA ATGCGAGTTG	180
GGGTGTGGGC CCCAACACAG AGAATTTCTGA AAAGAAATTC TACAGGGCAA TGCGAGTTGG	240
GGTGTGGGCC CCAACATGAG AGAAATTGGA TTCCCAATTT CTGACAGACA ATGCAAGTTG	300
GCGGGGGCCC CAACACAGAA GCTGGACGAA AATCCTTGAA CGAATGAATG TGGAATTGG	360
CGGGGGGCCA ACACAGAAGn TGACGAAAAT nCTnGAACCA	400

(2) INFORMATION FOR SEQ ID NO: 4092:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4092:

GCATTTCTCA TAACACAAGG AATTTCAACA AGTCCGGCTA CTGGATCACA AACTAAACCT	60
AATAAATTAC TTATCGCTAA TGCCATAGCG TGCCCGGATG CTTCTGGTGA TCCTCCGAAT	120
ATAGCTACTG CTGCAGCTGC GGCCATTGCA GATGCTGAAC CAACTTCAGC TTGGCAGCCA	180
CCTGTTGCAC CAGCTACACT TGCATTGTTT GCTACGACAC GCCCAAACAA TGCTGAAGTG	240
AATAAGAAAT CAATCATTGC TCTTCTGTTA AATCATGTGT TTTTCTAATT AAAAAGTGCA	300
CCGGGAATGG TAnCCGAGGG AAnCAGCTGT GGGCGTTGCA CAAATAATAC CCCATCGCAG	360
CATTTGACCT TCATTTGGTT GCAATGGGAA CCTTTGACTG	400

(2) INFORMATION FOR SEQ ID NO: 4093:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4093:

TGACTTACGT ACTGTTCAAC CAATCGATGT TGACACAATT GTAGCTTCAG TTGAAAAAAC	60
TGGTCGTGCA GTTGTAGTTC AAGAAGCACA ACGTCAAGCT GGTGTTGGTGCAGCAGTTGT	120
AGCTGAATTA AGTGAACGTG CAATCCTTTC ATTAGAAGCA CCTATTGGAA GAGTTGCAGC	180
AGCAGATACA ATTTATCCAT TCACTCAAGC TGAAAATGTT TGGTTACCAA AAAAAATGA	240
CATCATCGAA AAAGCAAAAG AAACTTTAGA ATTTTAATAC ATTTTAAAAG TTAACGAATT	300
AGCGTATTTT AGTCTCATTG ATTAA _n ATGA AATG _n G _n TAA TTTACGGAAT CCTA	354

(2) INFORMATION FOR SEQ ID NO: 4094:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4094:

CGTTAACATG AAGTTACGTT CTTTTATAAA AAGATTTAAA CGCGTTATTA ATCTTGTGAG	60
TGTTCTTTCG AACACTAGCG ATTATTTCTT ATGAATTCAA GCTTATTTAA AACTCTTTAT	120
TCACTCGGTT TTGCTTGGTA AAATCTATAT nTTACTTACT TATC _n AGTTT TCAATGTACA	180
AATAATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TGCGTGCAAA GCAGGCGCTC	240
TCCCAGCTGA GCTAAGCCCC CAAATAGG _n A TTAAATTAAT GGTGGGCCTA AGTGGACTCG	300
AACCACCGAC CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT A	351

(2) INFORMATION FOR SEQ ID NO: 4095:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4095:

ATTGTTGCGA CTGGCACACC CGAAGATATT GCTCAGACAA AGTCATCATA TACAGGAAAG	60
TATTTAAAAG AAGTACTTGA ACGAGATAAA CAAAATACTG AAGATAAATA AGATTAAAAG	120

AAGTGAAGGA TGTTATAATT TATCCTTCGC TTCTTTTAT TAATTTAGTA ATGAATAGTA	180
GAAAGAAAAG ATGCGTAAAA AGAATTATGT TAAGATAGGG TCAATCTAGA GTAGTTAAAC	240
ATAAATCGAA CTnGGAGTGG GACAGAAATG ATAAAGAATC ACTAATGATT TATTATGTAG	300
TGGTTCTTTG TCATTAGCCA CAGCTATTTG TGTACTTAAA AnTAGGTATG CCAGTGTGCA	360
CTCCTTGAGA GGAAATACTn ATTT	384

(2) INFORMATION FOR SEQ ID NO: 4096:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4096:

CTGCATCTTC ACAGGTAATA TGATTTACAC GAGTCTCTCG TTGAGACAGT GCCCAAATCG	60
TTACGCCTTT CGTGCGGGTC GGAAGTTACC CGACAAGGAA TTTCGCTACC TTAGGACCGT	120
TATAGTTACG GCCGCCGTTT ACTGGGGCTT CGATTTCGTAG CTTCGCAAA AGAGCCGACT	180
CCTCTTGAAC CTTCCAGCAC CGGGCAGGCG TCACCCTGAT GACATCACCT TACGGTTTAG	240
CAGAGACCTG TGTTTTTGAT AAACAGTCGC TTGGGCCTAT TCACTGCGGC TCTTCTGGGC	300
GTTAACCTn AAAGAGCACC CCTTCTCCCG AAATTnACGG GGTCATTTTG GCCGAGTTCC	360
TTAACGAGnA TTCGCTCGGT GCAACTT	387

(2) INFORMATION FOR SEQ ID NO: 4097:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4097:

CCACTCACAT TCACACATCG ATTCACACAC CGCACTCAGC ACTCAGnATA CCGCATTCAG	60
CATTCAGCAC AGCGnACTCA GACTCAGAAC AGCGATTCAG ACTCGGATAG CGACTCAGAC	120
TCAGATAGCG ACTCAGATTC GGATAGCGAC TCAGACTCAG ATAGCGATTC AGATTCAGAT	180
AGCGATTCGG ACTCAGACAG TGATTCAGAT TCAGACTCAG ATAGCGACTC AGATTCTGAC	240
AGCGATTCAG ACTCAGACAG CGACTCAGAC TCAGACAGTG ATTCAGATTC AGACAGCGAC	300
TCAGATTCAG ATnGCGACTC AGACTCAGAT AGCGACTCAG ATTCAGATAGCGATTCGGAC	360

TCAGACAACG ACTCAGATTC AGATAGCGAT TCAGATTTCAG

400

(2) INFORMATION FOR SEQ ID NO: 4098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4098:

TCGTACCTGA ACTACTTTGT ATTAAAATAG TTACAACGAT ACCTGCAATA ACACCTAATA	60
CTGGATTTGA TGTAATTTG TTTAAAATAT CTCGTAGCCT GTCTCCTGCT GATGCTTGAA	120
GCCCGTCTCC CATGATTTTT AAGCCGTAAA GGAAAATACC TAAACCACCT AAAAAGGAGA	180
AAATGACTTC TGTAACCGAC ATTTCCATTA TTTCACCTCA AATAAGCTTT ATATTTAGAT	240
TATCGCTTAT AATTGTAAAT TTAATGTAA GATTAGGTAA AATTATTTAA CAATATATGT	300
TATTTGTATA TGACTTGTA AATATGTCA CTTATTATGT AAATTTTCAG TGGTGnAAT	360
GGCCAGTTTG CCAAGCACTG GTTTGACCA _n ATGGnGGCA _n	400

(2) INFORMATION FOR SEQ ID NO: 4099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4099:

ATCCTTTTCC ACTTAACATA TATTTTGGGA CTTACCTGG TGGTCTGGGC TGTTTCCGGA	60
CCGAACACGG nACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATAAT TGGCATTTCGG	120
AGTTTGTCTG AATTCGGTAA CCGGAGAGGG CCCCTCGTCC AAACAGGGCT CTACCTCCAA	180
TAATCATCAC TTGAGGCTAG CCCTAAAGCT ATTTCCGAGA GAACCAGCTA TCTCCAGGTT	240
CGATTGGAAT TTCTCCGCTA CCCTCAGTTC ATCCGCTCAC TTTCAACGTA ATCGGTTCGG	300
TCCTCCATTC AGTGTTACCT GAACTTCAAC CTGACCAAnG GTAGATCACC	350

(2) INFORMATION FOR SEQ ID NO: 4100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4100:

TAGAACTTGT TGCCAAACAG CATGCTTAAT TTCAATATCT TCTTTGACTG CTTCGATATA	60
TAAATCAGCA TCATCATTTA CCAAGTCATC ATCAAAATTA CCATATGTTA AATGACTCGC	120
TAGATTTAAG TCGAATAGTA GGGCCGTTT CTTATCTGTA ATTTTATCGT AAGATTTTTT	180
CGCAATGAGA TTTGGATCGT TTTTGTCCAC TACAATATCT AATAGTTTTA CTTTAAGTCC	240
AGCATTCACA AAAAGTGCTG CCAGTTGGAG CGCCCATTTGT GCCTGCGCCA AGAACGGnTA	300
CTTTATTAAT TGGTCATAGT GAnTCCnCCC ATTTAGTTGA GGGATAAET AACCAT	357

(2) INFORMATION FOR SEQ ID NO: 4101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4101:

TAACTCAGGC TGGGGACATA AATCAATATT CTATGCTCTA CGAATTATAT TGGCAGTAGT	60
TGACTGGnCG AAAATGCGCT TGTAACAAGC TTTTTTCAAT TCTAGTCAGG GGCCCCAACA	120
CAGAGAATTT CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGAGGG CCCCACACA	180
GAAGCTGACG AAAAGTCAGC TTACAATAAT GTGCAAGTTG GGGATGGGCC CCAACAAAGA	240
GAAATTGGAT TCCAATTTT TACAGACAAT GCAAGTnGGG GTGGGACGAC GnGATAAATT	300
TTGCGAAAAT ATCATTTCTG TCCCACTCCC ATCAAAAGAA TGACAT	346

(2) INFORMATION FOR SEQ ID NO: 4102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4102:

AATGATGAAA ATCAATTAG CAAAGCAGGT AAATTAAGTG ATGTCGCGTC ATTTAAGGAA	60
GCGATTCACA ATCGAGAATC ACAAAGTACA ACTGGTATCG GCGAAGGTAT TGCCATTCCA	120
CATGCCAAAG TGGCCGCAGT TAAGTCACCA GCTATTGCGT TTGGTAAATC TAAAGCAGGC	180
GTAGATTATC AAAGTTTGGG ATATGCAACC AGCACACTTA TTCTTATGA TTGCAGCGCC	240
AGAAGGTGGC CCCAAACACA TTCTAGATGC TTTACTAAAG TTGnCTGGTA TTTAATGGG	300

ATGAAAATGT ACGTGAGGAA ATnTTACAT GGCTTCATCA nCTGAAGAAG TACTAGCGAT 360
CAT 363

(2) INFORMATION FOR SEQ ID NO: 4103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

GAGTGCAGCG GATAACATTA AACCGACGAC AnCTTTTTTA TG TTCAGGTT TAGCTGTGTG 60
ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC GGCCTGACAT 120
AAAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGa TCACCAAGTT GAGCAAAGAA 180
GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC CAAGTGCCGT 240
CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA ATCTTAAGAT 300
GAAGCCATAA rCAAAGTAC CsGTTGGcAC CTGTTtTCGT TACAAATCCA CCAACATGtK 360
AaTGCCGGTT TGTATGGTTG GCCCAAnTGA nAACATCATA 400

(2) INFORMATION FOR SEQ ID NO: 4104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4104:

AATTGAGAAT TTGTCGCTAT TTGTAAATTG TATCCTGGCT TAAGTTGGCC AAAGTGTCTT 60
ATTTTTTTAA AGTATTTAAA AGTAAAATTA CATGTTAATA CGTATATTAA TTGGCGAGAC 120
TCCTGAGGGA GCAGTGCCAG TCGAAGCAGG GGCCCCAACA CAGAAGCTGA CATATAGTCA 180
CTTAACAACA ATGTGCCGGT TGGGGTGGCT GAGACGGCAC CCTAGGAAGG GACCCGTCAT 240
CAAAAATTCT ATTTATAGAA TTTTACAGTA ATGTGCCAGA TGGGCATAGC GACCCATTCA 300
ATACGAnTAT nTGAnTAAAT AGAGAACAGC AGTAAGATAT TTTCTAATTG AAAATTAT 358

(2) INFORMATION FOR SEQ ID NO: 4105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4105:

GACGCGTTAC CAAATGCGG AATTAAAGCA AAATCTTCAA TTTCAATGAA CAATGTGACG	60
TATACGACGC AAGACGAACA TGGTCAAGTT GTTACAGTAA CAAGAAATGA ATCTGTTGAT	120
TCAAATGACA GTGCAACAGT AACAGTGACA CCACAATTAC AAGCAACTAC TGAAGGCGCT	180
GTATTTATTA AAGGTGGCGA CGGTTTTGAT TTCGGACACG TGAAAGATT TATTCAAAAC	240
CCGCCACATG GGGCAACGGT TGCATGGCAT GATAGTCCAG ATACATGGAA GGAnTACAGT	300
CGGTAACACT TCATAAACT GCGGTTTGTh ACCATTACCT AATnGTCAAG GGTACGGCGT	360
TAATGTTTGA AGGTTCCCGT TCCAAGGTTT TTTCCCGTTT	400

(2) INFORMATION FOR SEQ ID NO: 4106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4106:

GAAGTTAAGC TCCTTAGCGT CGATGGTAGT CGAACTTACG TnCCGCTAGA GTAGAACGTn	60
TGCCAGGCAG TTTTTTAATC AAATTTTGGT TAAAAAATAA AATGGACAAG ATAAAAAAG	120
TTATTGACTT AAATGTTAAT AAAATGTATA ATTAATTCTT GTCGGTAAGA AAAATGAACA	180
TTGAAACTG AATGACAATA TGTCAACGTT AATTCCAAAA AACGTAACATA TAAGTTACAA	240
ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTTCATGGGA GAGTTTGGAT	300
CCTGGGCTCA GGATGGAACG CTGGGCGGCG TGCCCTAATA CATGGCAAGT CnGAGCGAAC	360
GGGACGAGAA GGCTTTGCTT CTCCTGGATG TTAACCGGCn	400

(2) INFORMATION FOR SEQ ID NO: 4107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4107:

GATTGTGCCA CGCTTTTAAC CGAAATACAA CATCATCATT GACAATTTGT TGATTTGAAA	60
AATCTTTCTC TTCAATAAAT ACATACGTTT GCATCGTATG TGCTTTCATG TAACTCAATA	120

TTGGTTTTAA ATGCATTTCA GGAATTAAAT AATGTTTACT AGAACCTGCT GTCGCTACAA	180
GTCCTATTAC CTTGTCACGA AACGCATTGA CTGGAAGTAG ATCAAACACA TTTnnCAAAG	240
CACCAGGGAT GGAAAGCTTG AAAAATTGGA AAACCAATAA AAATCACATC AGCCTGCATT	300
AACGACGTCG TTAATTTATA TACATCTCCT GTAGTATCTA GnT	343

(2) INFORMATION FOR SEQ ID NO: 4108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4108:

ATACAAAACA CCAGGTCGTG AAGATAAACA ATCACAAGCG GCTACTGCTT CAGCAACTGA	60
ATTACCATAT GCAGTATTAG AAGCTATGGG TGGCAAAGCA AACATTAAAC ATTTAGACGC	120
TTGTATCACA CGTCTACGGT TGAAGTTAAC GACAAATCTA AAGTTGATGT TCCTGGTTTG	180
AnAGATTTAG GCGCATCTGG TGTATTAGAA GTCGGCAATAATATGCAAGC AATTTTTGGT	240
CCTAAATCTG ACCAAATCAA ACATGAAATG CAACAGATTA TGAnTGGTCA AGTAGTAGAA	300
AATCCTACTA CTATGGAAGA CGATnAAGAC GAAACTGTTG TGGGTTGGCA G	351

(2) INFORMATION FOR SEQ ID NO: 4109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4109:

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT	60
TTTTTAAATA CTAAAATACA TGTTGGAATA CTTGTCCCAT AGAAAATATT GGCTGGTAAC	120
CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGnAT CACACCTTCT	180
GCGGCACCAC GGAATAATAC ACCATGTGGG AGTACGACTG CnATGGTACC TTCATCGTCT	240
AAGGTAATGT ACCCTGTGGT TGAATAAAGG CAAAATCTGC TTTGGGATTT TGGCGCAACT	300
TTGCCCGTAA CCACTGAATC GTTCATCATT TTCAAATTTT TGAATCnGCT GGTCCATTCTG	360
CACTGTA	367

(2) INFORMATION FOR SEQ ID NO: 4110:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4110:

GTCGTCCGAT TGAAGGATGG AGTACTGTCG CATTTGGAA AGACTGGCAA GGACCACCAC	60
GTTTGCAAAA CGGAACAAGT TGGTTCTATT TTGCAACAGA CCAATGGAAA TATGAAGAGT	120
CAAATGTAGA TCGTTTAAAA TCTCCATTAG CTAAACAGA GGAGTTAAAG CATCAACATC	180
CAGCTGATTA TAATGTTTTA GCAGCTAGAC TTGGTTGGTT ACCATCATAT CCACAATTTA	240
ATAAAAATAG TTTGTTGTTT GCAGAAGAAG CTAAAGATGA AGGTATAGAT TCAAATGAAG	300
CGATTTTGCC ACGTGCAATT GATGAAGTGA ATCAAAACCA AACACCATTG GCCATAnGAA	360
AATCCTGATT TGGAAAAGGA TCCTnCCAAA ATCCAnnATT	400

(2) INFORMATION FOR SEQ ID NO: 4111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4111:

TCAGATGAAG CTAAAAGTAA AGGTATTACA TGTGCAAGTG CAGGTAATCA TGCTCAAGGT	60
GTTGCCTATA CAGCTAAAAA ACTTAATTTA AACGCTGTTA TCTTTATGCC AGTCACTACA	120
CCTTTACAAA AGGTAAATCA AGTAAAGTTC TTTGGAAATA GTAACGTTGA AGTTGTACTC	180
ACTGGTGATA CATTTGATCA CTGTTTAGCT GAAGCTTTA CTTATACAAG TGAACATCAA	240
ATGAACTTTA TAGATCCATT CAATAATGTT CATAAATTT CTGGACAAGG TACGCTTGCT	300
AAAGAAATGC TAGAACAAGC AAAGTCnGGA CAATGTTAAC TTTGATTATC TATTTGCCGC	360
AATTGGTGGT GCGGGTTTAA TTTCCAGTAT TAGTACTAAC	400

(2) INFORMATION FOR SEQ ID NO: 4112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 4112:

GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA GTCAAACGCT CACATACGGC	60
TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA	120
ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT	180
GAGTGTTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT	240
TATTCACCTCG GntTTGCTTG GGAAAATCTA TATTTTACnT ACTTATCTAG TnTTCAATGT	300
ACAAATAATG GTGGGCCCAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGGCGTGC	360
GG	362

(2) INFORMATION FOR SEQ ID NO: 4113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4113:

CAGGTGGTTT TGCGAAAAGT GAAGTATGGC GTCAAATGAT GTCAGATATA TTTGACACAG	60
AGTTAGTGGT TCCTGAAAGT TATGAAAGTT CATGCTTAGG TGCCTGCGTG CTCGGACTTA	120
AAGCTGTAGG TGACATTGAA GATTTTTTCAA TCGTTTCATC GATGGTCGGT GCCACAAACA	180
ATCATACGCC GATTGAAGAA AATGTCACCTG TTTACCAAGA GATCGTATCC ATTTTTATCA	240
ATTTAAGTCG TTCTTTAACA GAGAATTATG ACAAATTGCA GATTTCAACG CCACATATCG	300
CTGAAATAAA ACnCCATAAA TACGnCACTC AAGCATCTTA GATAAAGTTG TnGGCCATGC	360
TAC	363

(2) INFORMATION FOR SEQ ID NO: 4114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4114:

GGTCTGGGCT TGGTTCCGGT TCTGGGTCTG GACTTGGTTC TGGATCTGGC GTTGGTTCTG	60
GTTCTGGGTC TGGACTTGGT TCTGGGTCAA CCGGCGGCCC TGGAGTTGGG TCTTTCGGAT	120
TTACTGCTGA ATCACCATCA GCACTTCCAC CACCATACG TACAACATTC TCATTATTCC	180
AACCGAAAAT ACTGTAGTCT CTATTTGTGA CAGGATCAAC ATTTTCTTGA ATAACCTGAG	240
TTTTTAAGTT CTTACCTGTA TTGTCGTAAT GCCCTTCTAC TAATACTACA TATGTTTTAG	300

TAATATCACC AAATTAATAC TAGCTACATT GGATGCnCAT AATAGATCTA TTTTAAATGG 360
nCTGTACTCC TTAAGGTAGA GCATTGGACT GCAn 394

(2) INFORMATION FOR SEQ ID NO: 4115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4115:

GGCGATTATA TTAAAAAGCC AATTACAGAA TGTAGTGGTA ATGAAATATG CCAAGAATGG 60
CTGTATCACT TAGGTGTATC AACTGACAAA ATTGAAGACT TAGCAAAACA TGCATCTAAT 120
ACGATTCCCTG TTTATATGCC ATATATCACA TCTTATTTCA TGACGCGTGC TATCGGCGAC 180
AGACCTTTAG TCGTCCCGCA TCAATCTCAG AACTTAGCAT TTATTGGTAA CTTTGCCAGA 240
AACAGAGCGA GACACTGTAT TTACAACAGA ATATTCGGTT CGTACTGCCA GGGAAGCTGT 300
TTATCAATTA CTAAATATAG ATCGTGGTAT TCCAGAAGT ATCAATAAGT CCATTGGATC 360
TTnCGCGTnC TTAATGGGAT GGCCATATAC GAACTGGATG 400

(2) INFORMATION FOR SEQ ID NO: 4116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4116:

AACATATTTT AAGTAGGTGA ATGAATGGTA AATGAACAAA TCATTGATAT TTCAGGTCCG 60
TTAAAGGGCG AAATAGAAGT GCCGGGCGAT AAGTCAATGA CACACCGTGC AATCATGT 120
GCGTCGCTAG CTGAAGGTGT ATCTACTATA TATAAGCCAC TACTTGCGCA ATGTCGTCGT 180
ACGATGGACA TTTTCCGACT GTTAGGTGTA GAAATCAAAG AAGATGATGA AAAATTAGTT 240
GTGACTTCCC CAGGATATCA ATCCTTTAAC ACGCCACATC AAGTATTGTA TACAGGnAAA 300
TTCnGGGTAC GACAACACGA TTATAGGTTG TTAAGTGGGT TAGGTATTGA AAGTGTTTG 360
GTCnGGGCGA ATGTTTTCCA ATTGGGTAAA AGGCCCATGG 400

(2) INFORMATION FOR SEQ ID NO: 4117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 389 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4117:

```
AATAAAAAGG AACAAAACGA TGGCTATTGA TATGGACACA AATCATAAAT AGCTGCTTTG      60
TTCCTTTTTT AATTTATATA TTTAnAATAC ACATATCAA GAGCCTCGAG ATATAAGTCA      120
ATGTACTAGG CCACACAATT TAATATTGAC AGTAATTACC CGAACGAAAA TGCGCCCCGG      180
GGCCCCAACA TGGGGAATTT CGAAAAGAAA TTCTACAGAC AATGCAAGTT GCGGGGGCCC      240
CAACATAGAA GCTGGCCAAT AGTTAGCTTT CAATAATGTG CCAGTTGGGG TAAGGGCCCC      300
AACACAGAAG CTGGCCAATA GTCAGCTTTC AATAATGTGC CAAGTTGGGG TAAGGGGGCCC      360
CCACCACAGG GAATTTCGAA AGAAATnCT      389
```

(2) INFORMATION FOR SEQ ID NO: 4118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4118:

```
AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC      60
TGTGGATTAA TATTATGCCT GGCAACGTTC TACTCTAGCG GAAAnTAAGTT GACTACCATC      120
GACGCTAAGG AGCTTAACTT CTGTGTTTCGG CATGGGAACA GGTGTGACCT CCTTGCTATA      180
GTCACCAGAC ATATGAATGT AATTTATACA TTCAAACTA GATAGTAAGT AAAAGTGATT      240
TTGCTTCGCA AAACATTTAT TTTGATTAAG TCTTCGACG ATTAGTATTC GTGCAGCTCC      300
ACATGTCACC ATGCTTCCCA CCTCGAACCT ATTAAACCTC AnCATCTTTG AAGGGGATCT      360
TATnAACCGA A      371
```

(2) INFORMATION FOR SEQ ID NO: 4119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4119:

```
GCACTATTAG CCCAGTTAGA GAAAGATTGA CCTAATCTAT CCAACCAATC AGCCGACAT      60
```

TGAAACAGTG GTGCTAATTG CGGTGAATAC ATTGACTAAT CCGTCACCAA AACCACCTGC	120
AGCACTTAAT AGCTTGTTAA ATACCGAAAC ACCCGTTGTA TTCATCATAT TAAAGAATCT	180
TGAAGCTACA CTGCTATTTT CAGCCCATTn AAGCACGCTT TGAGACGCTT CTTCCATTCC	240
TCTTGAAATA CCACTAAAAA ACGGnTGTA GCTCTGCATT GCAGTTTTAA CAGTATTTAA	300
ACCATTTGCA AGAGTTGTGA AGnTAGCGGA TTGATTTTGC T	341

(2) INFORMATION FOR SEQ ID NO: 4120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4120:

GGTTGAGAAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCCTCCAC GTAAGCTAGC	60
GCTCACGTTT CAAAGGCTCC TACCTATCCT GTAAAGCTG TGCCGAATTT CAATATCAGG	120
CTACAGTAAA GCTCCACGGG GTCTTTCCGT CCTGTCGCGG GTAACCTGCA TCTTCACAGG	180
TACTATGATT TCACCGAGTC TCTCGTTGAG ACAGTGCCCA AATCGTTACG CCTTTCGTGC	240
GGGTCGGAAC TTACCCGACA AGGAATTTTCG CTACCTTAGG ACCGTTATAG TTACGGCCG	300
CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGAnAAACG CACTTCCTGT TAAACCTTTC	360
CAGCACCGGn CAGGCGTTCA CCCTnATTAC ATCAACTTTA	400

(2) INFORMATION FOR SEQ ID NO: 4121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4121:

AATAAATCTT GCTTTATTCT TTTTACCAGT AATATCTAAA TGAGTTGGAT ATTTAACTTT	60
CGCATTAATT TCAATATTAA ATTGCGTTAC CGCGACAAGC GCAAACACAA CATAcataAT	120
AAGATTGGCT AAAAAGATAT AGTTAAAGCT AAATTCTGCG ACAAAGCCGC CCATTGCAGC	180
ACCGACAGCC ACACCAATAT TTTGCGCTAA GTATATCGCA TTAAACGTTT GTCTTCGGCC	240
ATTTGGCCAC ACTGCTCCAG CCATAGCGTA TATCAGGA ATAATCATTC CGCCACCAAA	300
CCCTAACATT ACCAGGCCAT ACCAGCATAC CCAGGGCCAC CCGnGGAAGG AAATTAAGTA	360

GCGGTGGTAC TACCAAnGAC CAGTGAAGG TnCCAATTAA

400

(2) INFORMATION FOR SEQ ID NO: 4122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4122:

GATAACTAAT AAAGTTTAGT TAAGTATTTT AATAACAAGT AGTATGTCAT TCTATAGCT	60
AGAACAGATA TACTACTTGT TTGTTTTTGT GGAAAATTGA GTATATTCAA AAGGATAAGn	120
ACGAGAATTT CGTTATTAAA CTACGAATTC TCGATTTTTT TATATTTTAA GATAGGTTTA	180
TTTCTGAAAA CTTAATAGAA AGGGGTTTGA CAAAGCTAAA GTGAAGTTTG ACGgTATAAA	240
CGCAAATTAA ATATACTTTT ATAGAAAATT AACTCAGGCT GGGACATAAA TCAATATTCT	300
ATGCTCTACG GAGGTATATT GGCAGTAGTT GACTGAACGA AAnGCGCTTG TnACCAGCTT	360
TT	362

(2) INFORMATION FOR SEQ ID NO: 4123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4123:

AATTATTAAAG GTTGCTACAT GATAAATATC @CATGCATT TATCCACATG GTTGGTTTTT	60
CGCGAGGTGG TTTACAAGGA TTGTTGACAT TTCAAGACTT ACCAGTAACA AGTTATACAA	120
TCTGGGGTGG TGTCTCAGAT ATTGATTTAA TGTATGAAGA ACGTGTCGAT TTAAGAGGCA	180
TGCTACGAAG AATGATTGGT CATCCGAAAA AAGATCGAGC GGGCATATGA GGCACGCAA	240
GCGATTCCAA ACATTAATGA nAACAGTCCG CCAATATTAA TTGTACATnG GAGGGGAAAG	300
ACCCAGCAAG TTGGGTATTn CATCATGCGT ATTATTTTAA GCGGACCAAC TA	352

(2) INFORMATION FOR SEQ ID NO: 4124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4124:

AACCAGGTGA TCTACCCTTG GTCAGGTTGA AGTTCAGGTA ACACTGAATG GAGGACCGAA	60
CCGACTTACG TTGAAAAGTG GAGCGGATGA ACTGAGGGTA GCGGAGGAAA TTCCAATCGA	120
ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGC TAGCCTCAAG TGGATGATTA	180
TTGGGAGGTA GAGCACTGTT TGGACGAGGG GCCCCTCTTC GGGTTTACCA ATTTTCAGACA	240
AACTTCCGAA TGCCAATTAA TTTGAACTTn GGÆTTTCAGA ACATGGGTGA TAAGGTCCnT	300
GTTCGnAAh GGGAAACAGC CCAGACCACC AGTTAAGGTC CCCAAATGTA TGTTTAAGTG	360
GAAAAGGGTT TTGGCGTTGC CCCGACAACT AGGATGTTGG	400

(2) INFORMATION FOR SEQ ID NO: 4125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4125:

GGCTTATTAA TCAAAAATT TATAAGAAT ATGTAGAAA CTTTTATTTA CATGAGGCT	60
ACACGCTACA ACAGAAAATT AAAATTTTAA TTAGCTTATA CATTGTAATA GGTTTTTCAA	120
TTTATATGGT GGATGTTCTT GCAGTCCGTG TAGGATTAAT CATAATGGTT ATCATACAAA	180
CCGCTGTACT CTTTACATTT GTAAAAACAT TACCCAAATC AAATCATAAA ATAGAGGAGT	240
GATTGCCCAT GTTTATGGCA GAAAATAGAT TACAATTACA AAAAGGCAGT GCGGAAGAAA	300
CGATTGAACG TTTTACAAT AGACAAGGTA TTGAACTAT TGAAGGCTTC CAACAAATGT	360
TTGTCACTAA AACATTAAAT ACCGGGATAC AGCCGAGTAA	400

(2) INFORMATION FOR SEQ ID NO: 4126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4126:

AATCTATATT TTACTIONT ATCTAGTTTT CAATGTACAA TTTCTTTTTA GTCAAGCGCT	60
CGCATAAGCA ATATCACTTT AACCAAAAAA TATTTGAATG TTAAATAAAC ATTCAAACT	120
GAATACAATA TGTCACATTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA TATATCCTTA	180

GAAAGGAGGT GATCCAGCCG CACCTTCCGA TACGGCTACC TTGTTACGAC TTCACCCAA	240
TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGGTT ACTCCACCGG CTTCGGGTGT	300
TACAAACTCT CGTGGGTGTG GACGGGGCGG TGTGGTACAA nGACCCGGGG AACGTnATTC	360
AnCGGTAGCA TGGCTGGATC TAACGATTTA CTAnGCGGAT	400

(2) INFORMATION FOR SEQ ID NO: 4127:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4127:

CGAAATTTGT AGTAAAAGAT GTGCAACCAG CGAAACCAAC TGTGACTGAA ACAGCGGCAG	60
GAGCGATTAC AATTGCACCT GGAGCAAACC AAACAGTGAA TACACATGCC GGTAACGTAA	120
CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC	180
GTCGCAATAA TACGAGTCCA TGGGTGAAAG AGCATCTGC AGCAACTGTA GCAGGTATTG	240
CTGGAATAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GGATACAATT	300
CCAAGTTGGT TGCAACGCCA AGGAAGCGGA GAGACCAGTG AAGTGATTGA GCCACCGTAA	360
TGGTTGGnTT CCCAGTTTG TCGGCAnCCA CAACCGGAAC	400

(2) INFORMATION FOR SEQ ID NO: 4128:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4128:

GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT GGAGATTATC TGTCGTCTTC	60
AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC CATGTCAAAG TACCATTTGC	120
AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GCCTACGCGT TACATGAAAA ACGGAGAACA	180
AGCAGAACAA TTATTACGTC AGCTTATAGA AAAAGATGAA GCACTAGCTA AGTATGTCAT	240
GGGTTGTGAT GAAACAGCTT GGTGGTCATA TATGGGTCCA GATAATGATA TTTTCCAAGA	300
TCCATTAnGG CCATCTAACT GTTCCAGCTA AGGAAAGTAT CCCCGAAGTG GCTAAGCCCA	360
AAAATGATTA CGCCAACCAG CTAGTGGTCC ATnGCCAGC	400

(2) INFORMATION FOR SEQ ID NO: 4129:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4129:

AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA TAGATGGnGG AGGGGGGCAG	60
ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC	120
CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG GGTCGAACC	180
GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGG AGCTAATTCT CAAAATAAT	240
GACTCCTGAC GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGTGTTT TTGAACCGCT	300
TGGACCAAGG GAGCCATGGC TCCAACAGGT GAGGGACTCG AACCTnACGG ACCGATTCGG	360
TTnAACAGCC GGAT	374

(2) INFORMATION FOR SEQ ID NO: 4130:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 431 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4130:

TTTnACATGC ATCTGAATCT CTAATTTTAA AnAAATATGn ATATAAATAA GACAGTAAAA	60
ATTAAATTTT AGTTGTTGCA ATTTCTTCAT CTGTAGGTAC ATCATCGTTA AGGCCAACAA	120
GTGCTTCAGA AACATTTCTG GAATGATAAC CGATACGTTC AAGAACrCsA ATCATATCGA	180
TATATAGTAA TCCGCCTTTT GTTGTACATT CACCACGATT AAGGCGTTTA ATATGACCTT	240
TGCGTAGTTT ATGTTCAATA TTAAATGATT CTCTACTACG TTCTACAATT TCATCTTTTT	300
TCGTTTTGTC ATAAACATCT AACATGTCGA TGGCTTTATC AAATGACTCA GCAA AT GGT	360
TGGAATAAnT TATCCATACC GCGTTGTGCA TCTnCTGGTA ATGCGAATAT CTTCATCATG	420
TTGGCGGTTT T	431

(2) INFORMATION FOR SEQ ID NO: 4131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4131:

TTTAGTTGAA GGC	GGTGTGTTG TCG	CATTTGC TGT	TTGTTGC GGT	GCTTCTA CTT	TAGTTGA	60
GGGCGGTGTT GTC	CGGTTTG GTT	TTTGATTG CGG	TGCTTCT ATTT	TTAGTTG AGG	GC	120
GGTGTGTTG CTT	CCACTTT AGG	nAAATGA GTG	TTGTCGC GTT	TGCTGCT TGC	GTTGTCG	180
TTGTGATTAC ACCT	GTTGTT AAA	AAGGCCTA GTG	CTAAACT TGT	TTTAGCA ATC	GTTGTTA	240
TTTTCATAGT TGT	ATGCTCC ATT	CGTAATT AT	TAGATTTG TTC	GATACAT TC	ATTGAATC	300
ATACAGCTTT ATT	ATAGAGG CGT	ATTGCTC CAT	TCACATT AA	ACCTGnT A	ACCAGATTG	360
GAAGCAGCGT TGA	ATnAAAT GA	AAGAAAGCC AG	AAGTTTCGT			400

(2) INFORMATION FOR SEQ ID NO: 4132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4132:

CCATTC	ACTG TAT	GTCTTTG GCC	ACCACCT TG	ACGTTGTT GTT	GCTGTTG TG	ATTTTGA	60
TTAGCT	TGTT GTT	GATTTTG ATT	ATTTTGT GCT	TGATTGT TCG	CTTGATT AGC	GTTGTTT	120
TGATCAT	TAT CAG	ATTCATC TTT	AGTCGCT TT	GTCTTGAT CCT	CTTTTGA TTT	ATCACTG	180
TCTGTAG	ATT TTG	ATTTATC TTT	AGAAGCG TCT	TTAGATG TGT	CTTTGTC TTT	ACTTTCA	240
TCAGCAT	TAT TTTT	ATTTTGT ATT	CGCGATT TT	ATTTTCTT TT	GTACCATT ATT	ATGATTG	300
TTTAATG	CCA TGC	CTCCAAA TAT	CGCTAAA TGC	ACCGATA AAT	nAGTACA GCT	GCAATGA	360
ATGGTA	ACAA TAC	TTTGGGC CAG	nCACCGT TTTT	TACGGTn			400

(2) INFORMATION FOR SEQ ID NO: 4133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4133:

TTGAATACTT TTCT	TCCACA CAA	ATGTATA TCT	ATTGGCA TTAG	CTTCTA CTTTT	GTACC	60
ATCAATAAAA ATT	GAATTAT TAT	CAATAAG ATTT	TGCTTT AA	CATTGAC TAT	GGA	120
AATAAATAAA GAT	TCAATTA ACG	CATCAGT ATTA	GGATTC ACT	CTAAAAC GAT	TAA	180

TTTATAAGAA GGTGTTTGAT TTTGAGCTAA CCACATCATT CGAATACTGT CAGAAGTAA	240
TTTCTCTATT CTTCGACCAG AAAATACAGA TTGAGTATAT GCATATAAGA TGATTTTTTAA	300
CATCATTTTT GGGATGATAG GATGTTGCGC CACGATGATG TCTGAATTCA TCGAATTCGC	360
TAnCGGGTAC CGTTCACCA ATTCCATTAA CATATCGCGG AATATCATTT TGAGGAA	417

(2) INFORMATION FOR SEQ ID NO: 4134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4134:

GGTTTAATAT GGACCTTTGC CGTnTTTATG TTCAATATTA AATGGATTCT CTA CTACGTT	60
CTACAATTTT ATCTTTTTTC GTTTTGT CAT AACATCTAA CATGTCGATG GCTTTATCAA	120
ATGACTCAGC AACATGGTTG nAATAATTTA TCCATACCGC GTTGTGCATC TTCTGTAATG	180
CGnAATATCT TCATCATGTT GGTCGTTTTA ATTGAGCGAC ATACTCTTCT GTTAGCTCTG	240
CTACTTTTAA AATAGAGCGA TTGACATCAA ACATAACTGC TAAACGCTCA ACGTCTGCCT	300
TCGTAATGGC TTTTGTAGAA ATTCTAACTA AATAATTT CG AATGCTATCA TTGT	354

(2) INFORMATION FOR SEQ ID NO: 4135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4135:

CTGGGATCGC CACCTTTAAG TCTAACAACC TTGTTATATC GACGCGCTGCTCCACGATA	60
CAGTCATTTA TTTTTTCTTG CTGAATATGT TTTGCATACG GCTTTTTTACC AACATCGATA	120
ATTTTCAGTAG TCAAATTCGC ATATTGTAAA ATTAACGGAT TCACTAATCG ATCATATAGA	180
ATGACATCCG CTTACAGTAT TAAACGCTCA GCCTTTTTTCG TCAAATAATT CGGATTACCT	240
GGACCGGCAC CTATCAAGTA AACCTTGCCA TATTCCTCTA CAGACATATA TATACGGTCC	300
CGTCTGTAAC TTCTACCTCA TAAACATCTA CACAACCTTC ATCAGGTCTG GACAATACCT	360
GnATTAAACA ATTTTTGATC GTGGGGGGGC AAATACATAT	400

(2) INFORMATION FOR SEQ ID NO: 4136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4136:

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ACCACTGAAT CGTTCATCAT TTTCAMTTT TGAATCTGCT GTCCATTTCG CACTGTATGG      60
TGGGTTTCGCA ATAACCGCAT CAAATGTATT GCCTAAAAAG GCTGGATTTT CCAATGTGTC      120
ATCATTACGG ATCTCGAAGT TCTCATAACG CACATCATGT AATAACATAT TCATGCGTGC      180
TAAGTTGTAT GTAGTATTGn TACGTTCTTG TCCGAAATAA CGATACACTT GGTTCCTTT      240
ACCAACACGT AACAACAATG GAACCGGAnC CACATGTTGG GTCGTACACG TGGACGTAAT      300
TTATCnTTAC CGTGCTGTGA CAATCTTCGC CAGTATCTTA GATACTTG      348
  
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(2) INFORMATION FOR SEQ ID NO: 4137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4137:

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AGGTGGGGAT GACGTCAAAT CATCATGCCC CTTATGATTT GGGCTACACA CGTGCTACAA      60
TGGACAATAC AAAGGGCAGC GAAACCGCGA GTCAAAGCAA ATCCCATAAA GTTGTCTCTCA      120
GTTTCGGATTG TAGTCTGCAA CTCGACTACA TGnAAGCTGG nAATCGCTAG TAATCGTAGA      180
TCAGCATGCT ACGGTGAAAT ACGTTCCCGG GTCTTGTACA CACCGCCCGT CACACCACGA      240
GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTTAAG GAGCTAGCCG TCGAAAGTGG      300
GGACAAATGA TTGGGGTGAA TCGTAACAAG GTAAGCCGTG ATCGGnAAGG TCGGGCTGGG      360
AT .      362
  
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(2) INFORMATION FOR SEQ ID NO: 4138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4138:

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ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAT CTCTGGATCA      60
  
```

AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA	120
GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC CATTTTTATA	180
AGTCAAACGC TCACATACGG CTTCGTTTTT ATTATTTTAA ATGCTCATTT ACATAAGTAA	240
ACTCTGCTTT AAAATAATTT AACTGCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT	300
TTAAACGCGT TATTAATCTT GTGAGTGTTT TTTCGAACAC CAGCGATTAn TTCnTGAGGA	360
ATTCAAGCCT AnTTAAAACC CTTA	384

(2) INFORMATION FOR SEQ ID NO: 4139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4139:

CTCATTATGG GACGTGCACA AGA T GGTTTT CTTGATCAAG ACAAATATGA CATTATTTTC	60
AAAACAGCTG AAAATTTAGA CGTACCGATT TATCTACATC CCGCGCCAGT TAACAGTGAC	120
ATTTATCAAT CATACTATAA AGGAAATTAT CCTGAAGTAA CTGCGGCAAC ATTTGCTTGT	180
TTTGGTTATG GTTGGCACAT TGATGTCGGC ATTCATACAA TACATCTnGTnTnATCTGGT	240
ATTTTTGATC GTTATCCAAA GTTAAATATG ATTATTGGAC ATTGGGTGAG TTATCCCATC	300
TCCTTAGAAC GAATGGATGA AGCTTATCCG TGAACATTTG AACCACCCCG GAAGCAATAC	360
TTAAAAATAA ATTTAnTATC ACACCGGGTG GCATGGTACC	400

(2) INFORMATION FOR SEQ ID NO: 4140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4140:

CAACCACATT CGCTCGGCTC ACCTTAGAAT TCTCATCTTG AACTACCTGT GTCGGTTTGC	60
GGTACGGrCA CCTATTTTCT ATCTAGAGGC TTTTCTCGGc AGTGTGAAAT CAACGaCTCG	120
AAGACTCAAT GTCTTCTCCC CATCACAGCT CAGCCTTAAC GAGTACCGGA TTTGCCTAAT	180
ACTCAGCCTT ACTGCTTAGA CGTGCA T TCC AATCGCACGC TTCGCCTATC CTA T CTGCGTC	240
CCCCCATCGA TTAAAACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT	300

AAGCCTGTCG GGCTCAGCTT AAGGACCCGA CTAACCCAG AACCGGAAGA GCCTTCCTCT 360
 GGAAAACCTT AGTCAATCCG TTGGACCGGG ATCTCAACCG 400

(2) INFORMATION FOR SEQ ID NO: 4141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4141:

CATATCGATA ACATGACATA ACTCATGCTG GGTTTCCCCA TTCGGAAATC TCTGGATCAA 60
 AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 120
 TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA 180
 GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 240
 CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT 300
 AAACGCGTTA TTAATCTTGT GAGTGTCTT TCGAACATAG GCGGAGTATT TCTTAAGGAA 360
 TnCAAGCnTA TTTAAACTC TTAATCAGC GGTTTTGnCn 400

(2) INFORMATION FOR SEQ ID NO: 4142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4142:

GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTT 60
 TTTGTGTTTA CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA 120
 CTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATGT CGCTAAAGAC 180
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 240
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGGTTCGT CAGATTCAAA CGTTTCACTC 300
 GCCAAGCCAT TTTCTTGGG TTAATTTTAA TTTGACGTTT AAGGCATAAA AAAAAGAGAC 360
 TTGCGGGCTC AAATGCGGnT CATCGCATCC ATTTTTGnCn 400

(2) INFORMATION FOR SEQ ID NO: 4143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4143:

TTTAAAATTG ACATTATTAC TGACCAAACA AGTGACATG ATCCGCTAAA TGGATATGTG	60
CCACAAGGAA GCGAAAGTAT TGCGTGAAAA AGATCCGAAA AAATATGTTG AACTGTCACA	120
AGCTTCAATG GCAAAGCATG TTGATTAAAT GCTTGGAATT CAAAAACGT GGCGCTGTAG	180
CATTTGATTA TGGTAACAAT ATTCTGCAAG TAGCCTTCAA TAACGGAGnGn ATAAATGCTT	240
TTGGAATTCC CAGGTTTTGT ACCAGCTTAC ATTAGACCAT TnATTCTGTG TAGGTTAAAG	300
GGCCATTCCG CTTTGCTGCG TTGGAGTGGT GGATCCAAAA GATATCGAGCGTGCCGGATG	360
GAGGAAATG	369

(2) INFORMATION FOR SEQ ID NO: 4144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4144:

GGAAAGATAA ATAGCTTCAT CAATGTCATG CGTCACTAAA ATAATAGTTG ATTGCGTTTT	60
ATGTTTTAGT TGCACTAGTT GATCCTGAAG TTTATAACGT GTAAATGCAT CTAATGCACC	120
TAATGGCTCA TCCATCAATA TAACGTTAGG CTTATGCACA TGCGCTCGAC ATAGTGCCAC	180
ACGTTGTTTC ATACCCCCGG ACAGTTGCTC GGGAAAATGC TTTCCCCTGT CTTCTAAATC	240
AACTAATTTA AGCTGTGCnT TAATCTCTTC ATCACTAATT TTCTGTTGTA ATCCAATCCT	300
AATGTTGTCA TTAATCGTTT TCCAGGAGC AAATTATGGT GTTGAAATAG CATAAACAAAn	360
CGGGAGnGGC	370

(2) INFORMATION FOR SEQ ID NO: 4145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4145:

CGAGGTAGCA AAGAACAAAT TGCAGAAATAT GTACCTAAAT TACAGTCACA TGAAGTGCCT	60
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ACATGCTTTG CTTTAACTGA ACCAGAACAC GGTTCGGACG TTGCnGAGG TCTTGAAACA	120
GTCGCTGAAC GCCAAGGCGA TACTTGGGTT ATCAATGGTG AAAAGAAATG GATTGGTGGT	180
GCACATGTAT CTGATGTCAT TCCAGTATTC GCAGTAAATA AAGAACTGG GCAAACCCCA	240
TTGCTTTGTA GTCAGACCAG AACAAGATGG GCGTCGATAT TGAAGTCATT GGATAATAAA	300
ATCGCACTTC GGCATTGTTC CTAACGCCCT AATTTnAATT AAnTAATGTT CAAAGTAGGA	360
TTGAAGCGGG	370

(2) INFORMATION FOR SEQ ID NO: 4146:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4146:

TGGGGTGTTT TTACCAATAA AGCGTTGCAA GGTGGCGGTA GTTAAATCGA TTATGGTTGC	60
CACTTGTTAG CTACTAGGTA AAGATATGGT GCCGCATGAA GTCTAGGAAA AACATATAAT	120
CAATTGAGCA AACAACCGAA TCAAATTAAT GATTGGGGAA CATTTGATCA TACTAAATTT	180
GATGTCGATG ATCATGTTAC TAGTTATATG ACATTTGCCA ATCGAGCAAG CATGCAGTTT	240
GAATGTTTCGT GGTCTGCAAA TATCAAAGAA GATAAGGTTT ACGTTnTTT ATCAGGAGGA	300
GGATGGCGGT ATCCAATTTA TTTCCATTTG GAAATATATG GnGCCCCGTT TTGGGAACnC	360
ATTTTTTGGG AAGCCAAGCT	380

(2) INFORMATION FOR SEQ ID NO: 4147:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4147:

TACTTATCTA GTTTTCAATG TACAATTTCT TTTTAGTCAA GCGCTCGCAT AAGCAATATC	60
ACTTTAACCA AAAAATATTT GAATGTTAAA TAAACATTCA AAACCTGAATA CAATATGTCA	120
CATTATTCCG CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC	180
AGCCGCACCT TCCGATACGG CTACCTTGTT ACGACTTCAC CCCAATCATT TGTCCCACCT	240
TCGACGGCTA GCTCCTAAAA GGTACTCCA CCGAnTTCGG GTGTTACAAA CTCTCGTGGT	300
GTGACGGGCG GTGTGTACAA GACCCGGGAC GTATTCACCT GGCAGCTTGn CTGGGTTTAC	360

(2) INFORMATION FOR SEQ ID NO: 4148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4148:

CACCATACAT GCGAAATGGA CAGCAGATTC AAAATTTGAA AATATGAAC GATTCAGTGG	60
TTACGGCAAG CTTGCGCCAA AATCCAAAGC AGACTTTGCC TTTATTCAAC ACATGGTACA	120
TTACCTAGAC GATGAAGGTA CCATGGCAGT CGTACTCCCA CATGGTGTAT TATTCCGTGG	180
TGCCGCAGAA GGTGTGATTC GTCGCTATTT AATAGAAGAA AAGAACTACT TAGAAGCCGT	240
GATTGGGTTA CAGCCAATAT TTTCTATGGG nCAAGTATTC CAACATGTAT TTAGTATTAA	300
AAATGTCGCC ACAAGACGCC ACGTACTATT ATCGATGCAT CCAATGATTT GAAAAGGAAA	360
AATCAAACCA TTAAGCGTGC CAAGCGACGA TATnGCnCTA	400

(2) INFORMATION FOR SEQ ID NO: 4149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4149:

CAGCTATTGA TATCGATTAC CATACTGCTG TGGATAGCGA CAGGTTACAG TTGGAGGATA	60
CACTGAGTCC TCTGAGGAAT CAAATCCAAT TGA CTTTGAA GAATCTACAC ATGAAAATTC	120
AAAACATCAC GCTGATGTTG TTGAATATGA AGAAGATACA AACCAGGTG GTGGTCAGGT	180
TACTACTGAG TCTAACTTAG TTGAATTTGA CGAAGAGTCT ACAAAGTA TTGTAAGTGG	240
CGCnTGAGCG ATCATACAAC AGTTGAAGAT ACGAAGAATA TAACTGAAG TAATCTGATT	300
GAATAGTGA TGAATACCTG AAGAGCATGn TCAGCACAAG ACCAGTCGAG GAATnACTAA	360
AACCATCATC ATATTCnCAT CTGGTTAGGA CTGAAATGGC	400

(2) INFORMATION FOR SEQ ID NO: 4150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

```
AAGGACGACA TTAGACGAAT CATCTGGAAA GATAATCAAA GAAGGTAATA ATCCTGTAGT      60
CGAAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAGCACGTGA AATTCCGTCG      120
GAATCTGGGA GGACCATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCAGT      180
ACCGTGCAGG AGAAGGTGAA AAGCACCCCG GAAGGAGTTG AAATAGAACC TGAAACCGTG      240
TGCTTACAAG TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG      300
GCGAGTTACG ATTTGATGCA AGTTAAGCAT AAATGTGGAG CCGTAGCAGA ACnnGTTnTG      360
AATAGGCGTT A                                                    371
```

(2) INFORMATION FOR SEQ ID NO: 4151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4151:

```
TCAGCTTTTT TGATATGTAT TTTATAATGT ACAGCTCGTT GACnnTAATT TTCCTTATAT      60
TAAGTGCCAT CAATACAAA CCTAGCTCTC GTTTAACTTT ATTTATTCCT CGAACTGACA      120
TTCGAGTGAA CCCAAAATAG CCTTCATAAA TCCAAAAGCA GGCTCTACAT CAATTTTTTCT      180
TTGACTATAG ATGTTTTTTCG TTTCTGGTTC AGAAAGCTTT TGATTAATTT GGACTTTAAA      240
GTATTCCCAA TTATAATTCT TCATGGATTT TCTTATTGGG ATTTCGAATT TGGTTTCATG      300
CATTGATGTC TCAAAGAACA TGATGGAACA GTCCAnCACA TTCCAGATAG TTTGGAAGTC      360
TCGTTT                                                    366
```

(2) INFORMATION FOR SEQ ID NO: 4152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4152:

```
TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC      60
CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT      120
```

TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGÆTCAAA CGTTTTCACT	180
TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA	240
GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT	300
CTAGCGGGAC GTAAGTGGCT ACCATCGACG CTAAGAACCT TTCCTGGACT TGGTGGACAA	360
TCGChTGCCT CCTTCCTCCT CCTCGGGCTC TCGGCTTACG	400

(2) INFORMATION FOR SEQ ID NO: 4153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4153:

TGATATTCCT GTACCACCTA TAATCGTTTT AATCGATGGG GGGACGCATA GGnATAGGCG	60
ACGTGCGATT GGATTGCACG TCTAAGCAGT AAGGCTGAGT ATTAGGCAAA TCCGGTACTC	120
GTAAGGCTGA GCTGTGATGG GGAGAAGACA TTGAGTCTTC GAGTCGTTGA TTTCACACTG	180
CCGAGAAAAG CCTCTAGATA GAAAATAGGT GCCCGTACCG CAAACCGACA CAGGTAGTTC	240
AAGATGAGAT TCTAAGGTGG AGCGAGCGAA CTCTCGTTTA AGGACTCGGG CAAATGGACC	300
CCGTTACTTC GGGGAGAnGG GTGCTCTTTA nGGGTTTACG CCCAGAGAG CCGCATTGAA	360
TAAGGCCCAA GCGnTGTTTT ATCCAAAACA CGGTCTCTGC	400

(2) INFORMATION FOR SEQ ID NO: 4154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4154:

TTTTAGCAAT CATTTTAAACA GTCAGTCATA TTAAAGGCTG GCTAACGATT GTTATCTnGT	60
nCAGATTTGT AAGTTAAGAT TTCTTGTAAT GTGTATGCAG CACCATATGC TTCAAGTGCC	20
CATACCTCCA TCTCACCAA AC GTTGTCCA CCGAATTGCG CTTTACCGCC AAGTGGTTGT	180
TGTGTAACAA GTGAATATGG TCCTGTTGAA CGCGCATGTA ATTTATCATC AACCATGTGC	240
GCAAGTTTCA ACATGTACAT TACACCTACT GAAATACGGT TATCGAATGG TTCACCTGTA	300
CGTCCATCAT AAAGTACAGT TTACCATCA CGAGCCATAC CAGCTTCTTC AATTGTTGGA	360

CCATACATCG TCATCGTTTG CACCGTCAAA TACTGGTGGA

400

(2) INFORMATION FOR SEQ ID NO: 4155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4155:

GATCCGAAGT TACCAACAGG AGAGAAAGAG GAAGTTCCAG GTAAACCAGG AATTAAGAAT	60
CCAGAAACAG GAGATGTAGT TAGACCACCG GTCGATAGCG TACAAAATA TGGACCTGTA	120
AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCG AGAAAGAACG TAAATTTAAT	180
CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG TGAGAAGACA	240
ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA AGGTGAATCG	300
AAAGAAGAAA TCACAnAAGT CCAGTTAATG AATTAACAGA TTCGGTGGCG AGAAATACCG	360
C	361

(2) INFORMATION FOR SEQ ID NO: 4156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4156:

CAAAGTGACA GGTGGTGCAT GGTTGTCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC	60
CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATTAGTTGGGCAC TCTAAGTTGA	120
CTGCCGGTGA CAAACChGGG GnAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA	180
TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG CGAGTGCAAG	240
CAAATCCCAT AAAGTTGTTT TCAGTTCGGA TTGTAGTCTG CAATCGACT ACATGAAGCT	300
GGGAATCGCT AGTAATCGTT AGATCCAGCA TGGCTAACGG TGGAnTACGT TTCCCGGGGT	360
CCTTGTTACA CACCGCCCGT	380

(2) INFORMATION FOR SEQ ID NO: 4157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4157:

TGGAGAAGGA CCCAAAAATG TTGCCGTTTC AAGGTTATGT TTTACAACAT TTCGAACCTTA	60
TGGATGATGG ATTCTGCCAA GTTAAAATAA CTGAAGATGT ATTGGAGCAA TTCGGTATTC	120
AGCCAAATGA AGCATCTCAG TTTGTTAATA CAATTGCTGA CATCAAAGGC TTGAAAATAT	180
GGGTATTTGC AGTCGATGGA AGGTAATGAA ATCAGATGTC GATTACGTTC TAAAGGGCAA	240
TTGATTATT AATGATATTG CGCAGATTTT GGTGGCGGTG GTCATCCGAA TCGGTCAGGA	300
GTTTCAGTGG ACCAGCTGGG GTGGAnTTGA GCCACTTGCT ACCAGCTTTA CGGCACCAAA	360
ACTTnACTTA TAGGAAGGGG CCCATTCCAT CCAGGTGGGC	400

(2) INFORMATION FOR SEQ ID NO: 4158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4158:

AAATCTCTGG GATCAAATCT TACTTACAGC TCCCCAAAGnCATATCGTCG TTAGTAACGT	60
CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT	120
TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT	180
AAACGCGTTA TTAATCTTGT GAGTGTCTT TCGAACACTA GCGATTATTT CTTATGAATT	240
CAAGCTTATT TAAACTCTT TATTCACCTG GTTTTGCTTG GTAAAATCTA TATTTTACTT	300
ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGn n	351

(2) INFORMATION FOR SEQ ID NO: 4159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4159:

AGTTAAAGGA ACTTTTAAAG TG GTTGGCCG CCGTnATTGC CTTCTnACC TTTTGTCTCT	60
TCTCTTGtTA CTTTTTCTGT CCCTGGTGCT AAATCmGGAT TAAATTTACG TTCTTTCTTG	120
AATGGAATyT CTTCTTTTTT TACAATCGAG TCTCCTTTTA CAGGTCCATA TTTTGTTACG	180

CTATCGACCG GTGGTCTAAC TACGTCTCCT GTTCTGGAT TCTTAATTCC TGGTTTACCT	240
GGAACCTTCyT CTTTCTCTCC TGTTGGTAAC TTCGGATCAA ATCGTCTCG ATGACCTGGT	300
GTTATCGTTT CTGGTCCGTA TTCTGTAAAT TCATTAATCG GATCTTTTGT GATTTCTTCT	360
TTTGGTTCAC CnTtnACGAA TAATnACTCC AGTAAAGGAT TTTTAAAGTG TTGGTGTCGT	420

(2) INFORMATION FOR SEQ ID NO: 4160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4160:

ACGATAATGG TGACGGGTTA CAAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGTCCT	60
CCACGTAATC TAGCGCTCAC GTTTCAAAGG CTCCTACCTA TCCTGTACAA GCTGTGCCGA	120
ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC	180
TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAnTCGT	240
TACGCCTTTC GTGCGGGTG GAACTTACCC GACAAGGAnT TTCGCTACCT TAGGACCGTT	300
ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAAn TAACCACTC	359

(2) INFORMATION FOR SEQ ID NO: 4161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4161:

ATTGACTAAG GTTCCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA	60
GGCCGGnAAC GGTAGGGCGA TGGATAACAG GTTGATATCT CTGTACCACC TATAATCGTT	120
TTAATCGATG GGGGGACGCA TAGGGATAGG CGAACGTGTC GATTGGATTG CACGTCTAAG	180
CAGTAAGGCT GAGTATTAGG CAAATCCGGT ACTCGTTAAG GCTGGAGCTG TGATGGGGAG	240
AAGACATTGT GTCTTCGAGT CGTTGATTTT AACTGCCGA GAAAAGCCTC TAGATAGAAA	300
ATAGGTGCCC GTGACCGCAA ACCGACACAG GTAGTnCAAG ATGAGAAAnTC T	351

(2) INFORMATION FOR SEQ ID NO: 4162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4162:

AnCGTCCTGC TTTGCACGCC AGAGGTCAGC GGTTTCGATCC CGCTAGTCTC CACCATTTAT	60
TTTTTACACG ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT TCCAAAAAAC	120
GTAACATAAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT CATAATTTTT	180
ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA CATGCAAGTC	240
GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG AGTAACACGT	300
GGATAACCTA CCTATAAGAC TGGGGATAAC TTCGGGGAACCGGAGCCAAT ACCGGATAAT	360
AnTTTGAACC GCATnGGTCC AnAAGTGAAA GACCGGCTTG	400

(2) INFORMATION FOR SEQ ID NO: 4163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4163:

ATTTTATATA TGAAATAATC TGGGACAACA TTCATAAATC TTATTGTCGT CCATTTTTTTT	60
AAAATAATAC CAATCTCATT TTAAATTCT AACTTG GTT TCGTATAATA CGCTCTTAAA	120
TCTTTAAATT TAGGATTTAT TTCTGTTGGT ACTTGTTTTG TGGTTGGCGA TTGTGGTGTG	180
TCTGATTTAG TAGATTGCAT TGTTGTGGC GTGTTTGTG ATGGAGGTGT TGTCACTTTA	240
GTTGnAAGGC GGTGTTGTCTG CATTTGCTGT TTGTTGCGGT GCTTCTACTT TnATTGCAGG	300
CGGTGTTGTC GCGTTTGTT TTGnATGCGG TGCTTCTATT TT	342

(2) INFORMATION FOR SEQ ID NO: 4164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4164:

TCACGACACG AGCTGACGAC AACCATGCAC CACCTGTCAC TTTGTCCCCC GAGGAAGGGC	60
TCTATCTCTA GAGTTGTCAA AGGATGTCAA GATTGGTAA GGTTCTTCGC GTTGCTTCGA	120

ATTAAACCAC ATGCTCCACC GCTTGTGCGG TTCCCCGCA ATTCCTTTGA GTTTC AACCT	180
TGCGGTCGTA CTCCCCAGGC GGAGTGCTTA ATGCGTTAnT GCCAGCACTA AAGGGGCGGA	240
AACCCCCTAA ACACTTAGCA CTCCATCGTT TACGGCGTGG AACTACCAGG GTATCTAATC	300
CTGTTTGATC CCCACGCTTT CGCACATCAG GTCATTAACA GACCAGAAAT CGCTTGGCCA	360
nGGGGGTnCC nCCAAAACTT TGGGGATTTA ACGGTAAAAA	400

(2) INFORMATION FOR SEQ ID NO: 4165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4165:

TAATTATTTG CTATTTATAC GAAAGCAGAA TCTCCAGTCA AAGCGCGTCC AATTACTAAG	60
GCATTAATTT CATGTGTACC TTCGTACGTG TAAATCGCTT CTGCATCAGA GAAGAAACGT	120
GCAATATCAT AATCGTCAGC TAGTATGCCA TTACCACCTG TAATACCGCG GCCCATAGCT	180
ACTGTCTCAC GCAAACGTAA GGCATTCATC ATCTTCGCCG TTGAAGTTGC AACCTCGTCA	240
TATTCACCAT GTGCTTGCAT ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGAGCTAAA	300
TTAnCTTGCA TCATTGCTAG CTTTCCTGTA TTAACGGAA TACTAATnG GTTGCCGAAT	360
GCTTACGCTC AGGGACnTAA CnAAGTGGCA CGTAAGCGGC	400

(2) INFORMATION FOR SEQ ID NO: 4166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4166:

AAAGTTCTTT GGAAATAGTA ACGTTGAAGT TGTACTCACT GGTGATACAT TTGATCACTG	60
TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCA	120
TAATGTTTAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAGCAAA	180
GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT	240
AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG GAAAATTATA GGTGTTGGAA	300
CCTTCAGGTG GCAAGTAGTA TGGTATGGAA TCnGGTGGTG GGTAAATAAT CCnGGTnGTC	360
CACATTGGCC CTAATAACCG ATAAAATTTG GGGGGCCGGG	400

(2) INFORMATION FOR SEQ ID NO: 4167:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4167:

CTTATAATCC ACACCCTGAG CAAACGCTnC TTATGACAGA GTATTAAAAT AAGCCGATAA	60
AGATACACAC CTTTACCGAC TATTTAAAAT AACTTCACC AATTCATTTT AATTTAATGG	120
ATTGAAGTAA CTAAATTAAT ATTATGTTGT TCAATTAAAA GCTTCATACA AACCTAATCT	180
ATTTGCACTC CACCGGTAAC ACCGAACACT TGTCCGGTTG TATAACTTGA TTCTTCTGGA	240
CGCTTAATAG CACATAAGTT CCACATAACT CAACAGTTG ACCTGCACGG ACCTAAAGGT	300
GTTTTTTGTA CCAAATGnTT GGGGATTTTA CTTnGTGGGT TGTCCACCAG AAATTTGT	358

(2) INFORMATION FOR SEQ ID NO: 4168:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4168:

TTTCTTGACC ATATGGACGT AAAGAGATGT TAGCATCACA ACGTAAAGAT CCCTCTTCCA	60
TCTTAACGTC TGATACACCA GTGTATTGAA TAATTGAACG CAATTTTTTCT AAATATGCAT	120
ATGCTTCTTT AGGTGAACGA ATATCTGGTT CAGATACGAT TTCAATTAGC GGTGTACCTT	180
GACGGTTCAA GTCAACTAAT GAATACTCAC CTTTATGTGT TGACTTACCA GCATCTTCTT	240
CCATGTGGAA GACGAGTAAT ACCGATTCGT TTTGTTTCAC CGTCGACTTC GATATCGATA	300
TATCCATTTT CACCAATTGG TTGATCAAAT TGAGAAHTG AGAGCTTnTG GnTTAGCTGG	360
ATAGAAATAG TTCTTACGGT CAACTTAGAT CCGTTGCGAT	400

(2) INFORMATION FOR SEQ ID NO: 4169:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4169:

ACCATGTTTG AATGAATCCA TTGGAATCAT TATTGAAGTA AATTAAGGAA TCTATAATGT	60
TCGTTAAATA AAAGTATGCC CGTTGTGCTT CACACCCGAT AGATAGGGAT TTACAGAAA	120
ATTCAGGTCT CTTCCACGTC ATATTTGGAC CCATCGAAAA TTCGGGTTCT CAAATCATCG	180
AACATAACAA AAGAAGCTAA GCAACATGTA GGCCGTTGTC ACTTAACTTC TTGTTTTTCC	240
GATGACAGCT TCTATTTAGA GAATGTCATG ATTATTTTAT ATTCACTTCA ATGTTATCAA	300
TATTAGTGCC ATCTATGACA TCTGCCATGC GATTTTCTTG TAATTTTTTG TGCAATCAAC	360
GTGTACnTCC ACGGTTTTCA TTAAAnACA ATTTACCGGA	400

(2) INFORMATION FOR SEQ ID NO: 4170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4170:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA	60
TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGCGTAA CGATTTGGGC ACTGTCTCAA	120
CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG ACAGGACGGA	180
AAGACCCCGT GGAGCTTTAC TGTAGCCTGA TATTGAAATT CGGCACAGCT TGTTACAGGA	240
TAGGTAAGGA GCCTTTGGAA ACGTGAGCGC TAnTTTACGT GGnAGGCGCT GGGTGGGGA	300
ACTTACCCTA AGCTGTGTTG GCTTTCTAAC CCGCACCAnt TATCGTGGTG GGGAGACCAT	360
GGTCAAGCGG GGCATTTTGA ATGGGGGGCG GTTCG	395

(2) INFORMATION FOR SEQ ID NO: 4171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4171:

TACATTATAG CTTTAATCGT TTGAAGTATA GTTTGAAACC AGTAGTCACA GCTGTTCAAG	60
GTGCTGCCTT AGGCGGTGGC TGTGAGCTTG TACTTTACTC ACCTATTGTT GTCGCTGCAA	120
GTGAAACATA TATCGGTCTT GTTGAAGCAG GTGTTGGCTT ATTACCGAGT GGCGGTGGCC	180
TTGCAGAAAT GGCTGATCGC ATATTACGCA CATCGCATAA GTTTGATGAC AAACAAGCTT	240

CCATGACAAA AGTACTGACG AATATCGCAT TCGGAnGCT CTACAAATGC CTTTGAGGCA	300
CGTCGTATGG GTATTTACCG TGGATACAGA TACGATnATT TCCAATACAG CACAACGnGT	360
CGAAGTGGCG C	371

(2) INFORMATION FOR SEQ ID NO: 4172:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4172:

ATGGTGGAGA TAGCGGGATC GAACCGCTGA CCTCCTGCGT GCAAAGCAGG CGCTTCCCA	60
GCTGAGCTAA GCCCCATAA TAATTACAGT ATATCGGGAA GACAGGATTC GAACCTGCGA	120
CCCCTTGGTC CCAAACCAAG TGCTCTACCA AGCTGAGCTA CTTCCCGTAT AATTAACGCG	180
CCCGATAGGA GTCGAACCCA TAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG	240
CTACGGGCGC ATATGTTTTT ATTGAAAATn GTGCCGAGGA CCnGAATGAA CCGGTACGTG	300
ATCATTACCG CAGATTTTAA GTCCTGTGCG TCTGCCAGTT CCGCAnCCCG GACTATAAAA	360
T	361

(2) INFORMATION FOR SEQ ID NO: 4173:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4173:

GTACAGATGC ATTGTTAAAC AATCAGTTGC ACAGCTGTT GAAACTGGTA GAGTATCTAA	60
TGGTGATTTA ATCATTATTA CTGCTGGTGT ACCAACTGGT GAAACTGGAA CTACTAATAT	120
GATGAAAATC CACCTAGTTG GTGACGAAAT TGCTAATGGT CAAGGTATTG GACGTGGATC	180
AGTTGTTGGT ACTACGTTAG TTGCTGAAAC TGTTAAAGAT TTAGAAGGTA AAGATTATC	240
TGACAAAGTT ATCGTTACTA ACTCCATCGA TGAAACGTTT GTACCTTATG TAGAAAAAGC	300
TTTAGGCTTA ATTACAGAAG AAATGGTATT nCACACCCAG TGCCATGGTT GGTTAGGAAA	360
AGnAATCCCA CCGTTGTAnG	380

(2) INFORMATION FOR SEQ ID NO: 4174:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4174:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAG	60
CTGAGCTGTG ATGGGGAGAA GACATTGAGT CTTCGAAGTC GTTGATTTCa CACTGCCGAG	120
AAAAGCCTCT AGATAGAAAA TAGGTGCCCC TACCGCAAAC CGACACAGGT AGTCAAGATG	180
AGAATTCTAA GGTGGAGCGA GCGAACTCTC GTTAAGGAA CTCGGGCAAA ATGGACCCCG	240
TTAACTTCGG GAGAnGGGTG CTCTTTTAGG GTTAACGCCC AGAAGAGCCG CnTTGAATAn	300
GCCCAAGCGC TGTTTATCCA AAACACAGTC TCTGCTnAAC CGTAGGGGAT TGTATAGGGG	360
CTTACGCCTG CCCGGTGCCT GGAAGGTTTA AAAGGGTGGT	400

(2) INFORMATION FOR SEQ ID NO: 4175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4175:

AGCCATGGCT CAGCGAGGTA GGA CTACGACCGA TCGGTTAACA GCCGATAGCT	60
CTACCACTGA GCTACTGTGG ATTAATATTA TGCCTGGCAA CGTTCTACTC TAGCGGAACG	120
TAATTCGnAC TACCATCGAC GCTAAGGAGC TTAACTTCTG TGTTCCGGCAT GGGAACAGGT	180
GTGACCTCCT TGCTATAGTC ACCAGACATA TGAnTGTAAT TTATACATTC AAAACTAGAT	240
AGTAAGTAAA AGTGATTTTG CTTCGCAAAA CATTATTTTT GGATTAAGTC TTCGATCGAT	300
TAGTATTCGT CAGCTCCACA TGTGCACCAT GCTTnCCACC TCGAACCT	348

(2) INFORMATION FOR SEQ ID NO: 4176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4176:

CATTTTTTTTA AAATAATACC AATCTCATTT TTAAATTCTA AACTTGGTTT CGTATAATAC	60
--	----

GCTCTTAAAT CTTTAAATTT AGGATTTATT TCTGTTGGTA CTTGTTTTGT GGTGGCGAT	120
TGTGGTGTGT CTGATTTAGT AGATTGCATT GGTGTGGCG TGTGTGTTGA TGGAGGTGTT	180
GTCACTTTAG TTGAAGGCGG TGTGTGCGCA TTTGCTGTTT GTTGCGGTGC TTCTATTTA	240
GTTGAGGGCG GTGTTGTCGC GTTTGGTTTT GATTGCGGTG CTTCTATTTT AGTTGAGGGC	300
GGTGTGAnT GTGGTGCTTC CACTTTAGGG nAAGATnAGT GGTG	344

(2) INFORMATION FOR SEQ ID NO: 4177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4177:

CAGAACCTTG nAATGAATCG CGATGGAATA TCTCTATCTG nAAACAGATT TCTTTTTGTC	60
CGCCAATGGC CTTGGAATTG TTAAATAAA TCTATTTGCG CTTCTTTATC AATGTCATAA	120
CCTAATGCTT TTAACCTCTC TGAGAAGCGT GTTTACCAGA TAATTTTCCT AATGGAAGTT	180
CAGTCGTGCT TACACCAACA AGTTGAGGTG TCATAATTTC ATATGTTTCA CGATGTTTTA	240
ATACGCCATC TTGGTGAATA CCTGATTCAT ACTAAATGC ATTTGGCCAA CAATTGCTTT	300
ATTTCTAGGC ACTCGAATAC CTGCATATCT TGAnATTAAA TCCGAGGTTT TAGTTCCTCG	360
AG	362

(2) INFORMATION FOR SEQ ID NO: 4178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4178:

GGAGCTAATA CCGGATAATA TTTTGAACCG CATGGTAAAG nTGGAAAGAC GTCTTGCTG	60
TCACTTATAG ATGGATCCGC GCTGCATTAG CTAGTTGGTA AGGTAACGGC TTACCAAGGC	120
AACGATGCAT AGCCGACCTG AGAGGGTGAT CGGCCACACT GGAAGTGA CACGGTCCAG	180
ACTCCTACGG GAGGCAGCAG TAGGGAATCT TCCGCAATGG GCGAACTTn ACGGAGCAAC	240
GCCGCGTGAG TGATGAAGGT CTTCGGATCG TAAACTCTG TTATTAGGGG AGGACATATG	300
TGTAAGTAAC TGTGCACATT TTTGACGGTA CCTnATCAGG AAGCCACGGT TTAGTGGG	360

CCCAGAAGCC CCGGTTAATA CGTGGGTGGG nAAGGGTTTT

400

(2) INFORMATION FOR SEQ ID NO: 4179:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4179:

GTTGTTTCAG CAGCGACACA GTGTATTCA TTCTTAGAAA ATGATGACTC AAACCGTGCA	60
TTGATGGGTG CGAACATGCA ACGTCAAGCA GTGCCTTTGA TGAATCCAGA AGCACCATTT	120
GTTGGTACAG GTATGGAACA CGTTGCAGCA CGTGATTCTG GTGCGGCTAT TACAGCTAAG	180
CACAGAGGTC GTGTTGAACA TGTGAATCT AATGAAATTC TTGTCGTCG TCAGTTGGA	240
AGAGAACGGC GGTGAACAT GAAAGGTGGA TTAAGATCGC TATCCATTAG CTAAATTTAA	300
ACGTTCAAAC TCAGGTACAT GTTACAACCA ACGTCCAATC GTTGCCAGTT GGGAGATGTT	360
GTTGGnnnTA C	371

(2) INFORMATION FOR SEQ ID NO: 4180:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4180:

AAAGGGAATC GAATTTTCTT TCTCTTCCTC CGGGTACTAA GATGTTTCAG TTCTCCGGGT	60
GTGCCTTCTG ATATGCTATG TATTCACATA TCGATAACAT GACATAACTC ATGCTGGGTT	120
TCCCCATTCG GAAATCTCTG GATCAAAGCT TACTTACAAC TCCCCAAAGC ATATCGTCGT	180
TAGTAACGTC CTTTCATCGGC TTCTAATGCC AAnGCATCCA CCGTGCGCCC TTAATAACTT	240
AATCTATGTT TCCACCATTT TTATAAGTCA AACGCTCACA TACGGCTTCG TTTTCATTAT	300
nTnAAATGCT CATTTACATA AGTAAACTCT GCTTTAAAAT AATT	344

(2) INFORMATION FOR SEQ ID NO: 4181:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4181:

CCGTGATCGG AAGGTGCGGC TGGATCACCT CCTTTCTAAG GATATATTCGGAACATCTTC	60
TTCAGAAGAT CGGGAATAAC GTGACATATT GTATTGAGTT TTGAATGTTT GTTCATTCAA	120
ATTAATGGGC CTATAGCTCA GCTGGTTAGA GCGCACGCCT GATAAGCGTG AGGTCGGTGG	180
TTCGAGTCCA CTTAGGCCCA CCATTAATTT AATACCTATT TGGGGGCTTA GCTCAGCnGG	240
GAGAGCGCCT GCTTTGCACG CnGAGGTCAG CGGTTGATC CCGCTAGTCT CCACCATTAT	300
TTGTACATTG AAAACTAGAT AAGTGAnGTA AAAATATAGA TTT	343

(2) INFORMATION FOR SEQ ID NO: 4182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4182:

CAGAGCCAAC TCGTATGTGA TTTGTCTGCG CCAATGTATG CATCATCAAA AGTTCTGGAC	60
TACTACACGC AAACGCTGGT ACATTATGAT GTTCCGTAAA CCAAATTCGC TTAAAGCCAA	120
GTCGATCTGC TAATTTTGCA AGTGTCCTG AATCTTGCAA TGCCTTTTGT GCATCCTTAC	180
CTTCATCTAT TAAGGCATAG TCTAATACGC TTAATTTAAC CAATCCGTCA TCTCCAAACT	240
TATCCTGTCA TGTCAAACCG ACATAACATT TTAGCGTCTT AATACCATTCT CTCTTCATA	300
TACCCACGTA TATGATAACG TTTTCAATAA CTTTATATCT TTCGCCTTAT TTnCTTTTCA	360
TATCATATTT CAGACTACAA ATGCATCATA GTTAATTAAA	400

(2) INFORMATION FOR SEQ ID NO: 4183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4183:

AAAGTATGAA AGATGGTAGT GACGCGGTTG GTGATTGGGC TGTATTGAAT GCACTCATTA	60
ACACAGCTGC AGGTGGTTCA TGGATTTTCA TCCATCACGG TGGCGGTGTT GGCATGGGAT	120
ATTCACTTCA TGCGGGTATG GTTGTTGTAG CAGATGGATC AGAGCGTGCT GAAGGAAGAT	180
TGGAACGTGT ATTGACGACT GACCCAGGTA TGGTGTGTCG CGACATGTTG nATGCTGGCT	240

ATGACATCGC TATTCAAACA GCTAAAGAA AAGGTATTCA nATTCCAATG ATTGGTGAAA	300
GCAGGTGATA AGTAATGAAT GATTTAATAT TAATCAnATA GCAGAnTATT TTTACCGGGT	360
CCAACAGATA AACCTTTGAA GGGTTAGGTA TTAGATGCAT	400

(2) INFORMATION FOR SEQ ID NO: 4184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4184:

TTCCTGTGC ATCGGCATCA CTATTATTAG CATGACTCAA TTATTGGGT CACAATATGT	60
CATTGCAGTT ATCATTGGTT TCGTCATATG TGCGATAGGT AATGGTTTAG TCGCAACACC	120
TGGAATTACG ATTGCAATTT TCAGTATGCC TAATGAnAAA GTTGGTTTAG CTACAGGATT	180
ATATAAAATG AGTGGTACAT TAGGTGGCTC CTTTGGTATA GCACTAAGTA CTACAGTTTT	240
CAGTATGTTA CAACTAACT ATGCACCAAG TGTAGCTGCA ACCGTAACAT TTATAGTCAG	300
CATTGTATTG ATGnTCCTTG GGnCATTTG CTGCATACAT GA	342

(2) INFORMATION FOR SEQ ID NO: 4185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4185:

AAGCATACTC TGAAGCGGTG AACAAAAATA GAACAGATCA CATTAGACAT TTAATTGAAT	60
TTAAAGCATG TACACCGATT GACATCGACC AAGTTGAACC GGTAAGTGAC ATTGTCAAAC	120
GCTTTAATAC AGGGGCGATG AGTTATGGAT CGATTTTCAGC GGAACACATG AAACGTTAGC	180
ACAAGCCATG AACCAATTAG GTGGAAAGAG TAATAGTGGT GAAGGTGGCG AnATGCAAAA	240
CGTTATGAAG TACAAGTTGA TGGAAGCAAC AAAGTAAGTG CGATTnAACAAGTTGCTTCT	300
GGGCGTTTTG GTGTACTAGT GATTATTTAC CACCTGCCAA GGAATTCCAA TTAAnACTTGC	360

(2) INFORMATION FOR SEQ ID NO: 4186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4186:

CCCAAGCGGA ATTCTAAAT GATCGTCGCT CCATTCTTCA TTTTAATAAA TCCAAACGCA	60
GAATCTTCAA CTGTAAATTC ATCTGGATTC CATGAACCCC AAGCGTTTGC CGCATGATGC	120
TGTTTATTTA ATTTATGGAA TGTTGAACCC ATCACTGATT CTGGTTCATA ATTATCCATC	180
ATCCATAACG TTAAATCTAA AGCGTGTGTA CCGATATCGA TTAATGGTCC TCCACCTTGG	240
AGCTTCTTCG TCTAGAAAGA CACCCCATGT TGGTACTGCT CGACGACGAA TGGGCATGTG	300
nCTTTCCGAA GTTAAATGTC TCCTAGTCG CCACGTTGGC GCTGCCTGGA TGGAAAATTG	360
GACGATCTGC TCGGGAAACG AATTTGGATA AACnGATGGG	400

(2) INFORMATION FOR SEQ ID NO: 4187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4187:

GAATCATCTG GCAACnCCC CCAAAGAAGG TAATAATCCT GTAGTCGAAA ATGTTGTCTC	60
TCTTGAGTGG ATCCTGAGTA CGACGGAGCA CGTGAAATTC CGTCG E ATC TGGGAGGACC	120
ATCTCCTAAG GCTAAATACT CTCTAGTGAC CGATAGTGAA CCAGTACCGT GAGGGAAAGG	180
TGAAAAGCAC CCCGGAAGGG ATGTGAAATA GAACCTGAAA CCGTGTGCTT ACAAGTAGTC	240
AGAGCCCGTT AATGGGTGAT GGCGTGCCTT TTGTAGAATG AACC GGCGAG TTACGATTTG	300
ATGCAAnGTT AAGCAGTACA TGTGGAGCCG TAGCGAAAGC GAnGTCTGA	349

(2) INFORMATION FOR SEQ ID NO: 4188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4188:

TGGATCCTGA GTACGACGGA GCACGTGAAA TTCCGTCGGA ATCTGGGAGG ACCATCTCCT	60
AAGGCTAAAT ACTCTCTAGT GACCGATAGT GAACCAGTAC CGTGAGGGAA AGGTGAAAAG	120
CACCCCGGAA GGGGAGTGAn ATAGAACCTG AAACCGTGTG CTTACAAGTA GTCAGAGCCC	180

GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT TTGATGCAAG	240
GTTAAGCAGT AAATGTGGAn CCGTAGCGAA ACGAGTCTGA ATAGGGCGTT TAGTATTTGG	300
TCGTAGACCC GAAACCAGGT GATCTACCCT nGGTCA	336

(2) INFORMATION FOR SEQ ID NO: 4189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4189:

CAAAGGATGT TAAGAAATAC AATTTATTAC CCAGCATTTA ATAATGGTGC TATAGAAGGA	60
ATTAATAATA AGATAAAATT AATCAAGTGA ATTTCTTTTG GTTACAGAAA TTTCAACAAC	120
TTTAAAGCAC GTATAATGAT GATTTTCAGC TTGTACAAAG GAGAAAAAAA GAAGACAACC	180
AAGCCCAATA ATGGACTGGC CGCCTAATAA TAAAAGCTCT AAAAGTTGTA TTTTAAAAAT	240
AGTTCTTTAA ATTATATACC CACCACATTT GGTGGAGGAC CTAAAAAAA GCACTTCCCC	300
AAAAATGGGA AAGTGCAAGT AGTGAGCCnT AGGAGGGTTC GGACCCTCTn nCCCCCTCT	358

(2) INFORMATION FOR SEQ ID NO: 4190:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4190:

TCACCAAGTT GAGCAAAGAA GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT	60
AAAnGTACCAC CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT	120
GGACCTAACA ATCTTAAGAT GAAGCCATAA ACAAAGTAC CGATGGCACC TGTTTTCGTT	180
ACAAATCCAC CAACATGATA AATGCCGGCT TGTATGCTTG GCCAATGAA AAACATCAAT	240
ACACCTAAAA AGATTGCGGC AAATGCTGTG ACAATAGGGA CAnATGTAGA GCCACCAAAG	300
AAACCTAAAT ACGGTGGTAA TACCATTTGT GnTATTTGTT GTGAAGTATT GCGGTCATAA	360
TA	362

(2) INFORMATION FOR SEQ ID NO: 4191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

TGATCACCCA TGTTCTGGAC TCCCAATTGA AATTGAATTG GGCATTGCGA GTTTGTCTGG	60
nATTCGGTAA CCCGnGCAGG GTCCCCTCGT GCCAAACAGT GCTCTACCTC CAATAATCAT	120
CACTTGAGGC TAGCCCTAAA GCTATTTTCGG AGAGAACCAG CTATCTCCAG GTTCGATTGG	180
nATTTCTCCG CTAACCTCAG TTCATCCGCT CACTTTTCAA CGTAAGTCGG TTCGGTCCTC	240
CATTAGTGT TACCTGAACT TCAACCTGAC CAAGGTAGAT CACCTGGTTT CGGGTCTACG	300
ACCAAATACT AAACGCCCTA TTCAGACTCG CTTTCGCTAA GGCTCCACAT TTA CTGCTTA	360
AC	362

(2) INFORMATION FOR SEQ ID NO: 4192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4192:

CGTGTATTAT GCCTTCTACA TTGGCCATTA TGAAAACTTA TTATCAGGGT GCTGAACGTC	60
AGCGTGCCTT AAGTTATTGG TCTATCGGTT CTTGGGGTGG CAGTGGTATC TGTTCACTCT	120
TCGGTGGTGC AGTTGCGACA ACTATGGGTT GGAGATGGAT TTTATCTTC TCAATTATCG	180
TTGCCGTACT TTCAATGTTA CTCATCAAAG GGACGCCTGA AACGAAATCA GAAATTACCA	240
ATACACATAA ATTTGACGTT GCAGGGCTAA TTGTTCTAGT AGTATGTTGC TAAGTTAAAC	300
GTTGTCATTA CTAAAGGTGC AGCACTTGGn TACACATCAT TATGGGTCTT GGGTTGAATG	360
CCAATCGGAA ATTGTAGCAT CnTTAATTTT CTAAAAGGTG	400

(2) INFORMATION FOR SEQ ID NO: 4193:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4193:

AATCCCATGG ACCCTCAAAT TCTTTATCTA AATAGTACCC TAATGAAGTT TTTCTGTGCA	60
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TGTGATTAAT TTCATGTAAA CCGATGACAC CAACTAGCGT TCCTTCATAC CAAATGCCAC	120
ACTGAAATCC ATTACCATCA GCAAATTGCA AAAGTCCTCT TTAATAAAT GCACGCGTAT	180
CTGATGGTTG CTCAGTTGCA TCTACCCAAG GTAACCATTC CCTAAGTGAA TTTCTTGAAC	240
GATTGACTAA ATTGAAAAGC GCTTCTGTGT CATGAGCTTC TAAAATTTTA ATGTTATTGT	300
TCAATCACTT TCATTCCAAA CATAChATCA CATCCTCATT CATThTCATA TAATCCGGnA	360
ATGACCATAT GAT	373

(2) INFORMATION FOR SEQ ID NO: 4194:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4194:

ACAAAGGACG ACATTAGACG AATCATCTGG AAAGAGAATC AAAGGTAATA ATCCTGTAGT	60
CGAAAATGTT GTCTCGAGTG GATCCTGAGT ACGACGGAGC ACGTGAAATT CCGTCGGAAT	120
CTnGGAGGAC CATCTCCTAA GGCTAAATAC TCTCTAGTGA CCGATAGTGA ACCAGTACCG	180
TGAGGAAAAGG TGAAAAGCAC CCCGGAAGGG AGGTGTAAAT AGAACCTGAA ACCGTGTGCT	240
TACAAGTAGT cAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGAAT GGAACCGGCG	300
AGTTtACGAT TTGgAttGCA AGGTTAAGCA GTAAATGTGG GAGCGTA	348

(2) INFORMATION FOR SEQ ID NO: 4195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4195:

AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAACGCCTG GCAACGTTCT	60
ACTCTAGCGG AAnTAAGThG GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG	120
CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA	180
TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAG	240
TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGAACCTAT	300
TAACCTCATC ATCTTTGAGG GATCTTATAA nCGAGTTGGG	340

(2) INFORMATION FOR SEQ ID NO: 4196:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4196:

```
TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAAATTAA TGAAAGATAC AGTAGGTGCT      60
GATGTAGAAG TAAAAGCATC AGGTGGCGTA CGTAATTTAG AAGATTTCAA TAAATGGTT      120
GAAGCAGGTG CGACACGTAT TGGTGCGAGC GCnGTGTTCA AATTATGCAA GGTTTAGAAG      180
CAGATTCAGA TTACTAATAT ATATnAATnT TGGGAGTGATAGCTATGACA AGACCATTTA      240
ATCGTGTACA TTTAATCGTA ATGGATTCAG TAGGTATTGG TGAAGCGCCA GACGCAGCTG      300
ATTTTTTAAAG ATGGAGGTTT ACATACTTTT A      331
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(2) INFORMATION FOR SEQ ID NO: 4197:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4197:

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GTAGACGTCC CGATAGCCGT TACGCATGGT TACGATGTGT ATTGGTGTCG GCATGGGTGC      60
AGCTGCTATA TTTGAATATG TGCGTTAGAA TGTTGATTTT TGGATGAAGC GGATTCGTTT      120
TGTTATTGAA TGAAGTAGGC TGAAGTTGAA GCCAGTTGAA GTTGAAGCGG GTTGAAGCAA      180
TTTCGTTTTTA TTGAATGAAG CTGTGTGAAA TATAGTGATT GAACAAAAAA AGTGGTTTTAA      240
TGGGATGGTG GTTATTTCG TTTTAGAATT TAACATTTAC ACGTCTAATT TTAAATCATT      300
GTTTTAAATT TTATGAATCG AAGCCCTTTG GATTTAATn TATTGCTAAT GCnAGTAACT      360
nATCTGATTG T      371
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(2) INFORMATION FOR SEQ ID NO: 4198:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4198:

GCGACCCCAA CCTTGGCAAG GTTGTnATTC TACCGCTEAA CTA CT TCTGC ATATGCGGGT	60
GAAGGGAGTC GAACCCCCAC GCCGTAAGCT nAGnATCCTA AGTCTAGTGC GTCTGCCAAT	120
TCCGCCACAC CCGCAAATGG TGAGCCATAG AGGATTCGAA CCTCTGACCC TCTGATTAAA	180
AGTCAGATGC TCTACCAACT GAGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA	240
ACCCCCAACC TACTGATTAC AAGTCAGTTG CTCTACCAAT TGAGCTAGGC CGGCAATATG	300
TAAGAATAAA TGGTGGAGAA TGACGGGTTC GnACCGTCGA CCCTGTGCTT GTTAAGGCAG	360
ATGGTTTTTCC CACTGGGGTA AATTTTCCGA TTTAAAAATG	400

(2) INFORMATION FOR SEQ ID NO: 4199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4199:

ATCAGTTGCT GTTGCGCCTT GTGGTAATGA ATTTACTAGT CGTACACCAA TAACCTCTGG	60
AATTGGGAAA TAAGAAGGTT GTCCAAGCAT TCCAGCTTCA GCTTCAATAC CACCAACACC	120
CCATCCTAGT ACGCCAATAC CATTTATCAT TGTTGTATGT GAATCAGTAC CAACTAATGT	180
ATCTGGAAAT GCAGTTTTTTT CACCATCTAC ATCACGAAØ TGTACAACAC TTGCTAAATA	240
TTCTAAGTTA ACTTGGTGAA CTATTCCAGT TGCAGGAGGG AACTGCATTG TAATTATCAA	300
ATGCTTTTCGG TTGGCCCAAT TTAAAAAACT GGATAACGTT CATnGTTACG TTCCAATTCC	360
TAATTTCCnA ATTACGGTTC CAnGAGCTTC TGGGATTTTG	400

(2) INFORMATION FOR SEQ ID NO: 4200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 4200:

CAACCTTTAT TGGTAAAAAC ACCCCAGCCA GGCAC TT TAC GCCTACGCAT CGCTTGTACA	60
CGTGCTACTA nAGGTTTACC AACCACACCT GATTCAATTG CTTTTTTAGC AGTAATTGCC	120
ACATCTGTGT GACGATAATG ATATGCGACA GTTAATAATT TGTGATTTTT ATTAGCCGCT	180
TCAATCATGC GATCACACTC TTCCGTCGTC ATCGCCATTG GCTTTTCACA CAATACATGG	240
CACACCATGG TTCAATGChT CTATAGAAAG ATCAGCAGGA ATTTATTAGG TGTACAAATG	300

ACCCATCAAC AAGTTTAAAC AGCTCGCTAG GTGnC

335

(2) INFORMATION FOR SEQ ID NO: 4201:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4201:

ATGATGTGGC GGTGGTGAAA TCAGACCGAT ACCTGCGTT GACCCTCTTG TCTTCGCAAT	60
CCACGGATAT ACCTTAGTAC CAGGTAATTG ACCACCTTCA CCAGGCTTTG CACCTTGCGC	120
AACTTTAATT TGAATTTCTT TGGCATGTTG TAAATAATCA CTAGTTACAC CAAAACGCCC	180
AGAAGCAACT TGTTTAATCG CACTTACTTT GTTGCTTCCA TCAACTTGTA CTTCATAACG	240
TTTTGCATCT TCGGCAACTT CACCACTATT ACTCTTTCCA nCTAATTGGG TCATGGGCTG	300
TGCTAACGTT TCATGTGCTT CCGnTGnAAT CGATCCATAA CTCATCGGCC CCGTATTAAA	360
GCGGTTGGAC	370

(2) INFORMATION FOR SEQ ID NO: 4202:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4202:

CAGCTAGCGA CTTACCTTGA CGTTTTGnGT ATTCATTCCA GCTTTGTnGG AATGAGtCGG	60
gATATAAGCA TCTTTAGATA ATGCACCATC AACTAATGGA TATTTATGTC CAGTTGGaGC	120
CAGAAATCAT AAACGTCTTC AGTGTAAGCA ACAGCATCTT CaTTTAATGC CAAAATGCTT	180
GGaTTAgTGC AATAACCATC GCAACTGnGC CAnACCTGT GTTGGCTCGC CGCCTGAATT	240
CAATCCATAA CGTGCTGTAT CTGTAGCAAT AACTAATACT TTTTCATTCG GTCTAGTTGC	300
TAAATAATCT TTAGCTAATT GAATTGCTGG TGTTGCAGCA TAACAAGCTT CTTTCATTTT	360
AAAGCAGCGT GCAAAAGGTT	380

(2) INFORMATION FOR SEQ ID NO: 4203:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4203:

TGCTCCATTT CTCACATTTG GTATTTCAAA GGTATACCAA GTCGTATGGG ATTATTACTT	60
GACATGTCAC CAAGAGCATT AGAAGAAGTT ATTTACTTTG CTTCTTATGT TGTGTAGAT	120
CCAGGTCCAA CTGGTTTAGA AAAGAAAAC TATTATCTG AAGCTGAATT CAGAGATTAT	180
TATGATAAAT ACCCAGGTCA ATTCGTTGCA AAAATGGGTG CAGAAGGTAT TAAAGATTTA	240
CTTGGAAGAG ATTGATCTTG ACGAGGAACT TAAATTGTTA CGCGATGAGT TGGGAATCAG	300
CTACTGGGTC CAAAGACTTA CTCCGTGGCA ATTAACGGTT TAGAAGTTGT TnGAATCATC	360
CCGTAATCCA GGGTACCACC CTCCnnGGnT GGATTTAG@	400

(2) INFORMATION FOR SEQ ID NO: 4204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4204:

AAATTCTTCC GCCCTGTAAT TCCTTAACCG CTTCAACGGC ATCGTnAATn TCTTACATTT	60
AGATAAAGAT GCATTGCAAG ATATCGTCAA CTTATTATTA GACGATGTAC AAGTTACATT	120
AGACAAAAAA GGTATTACGA TGGACGTTTC TCAAGATGCG AAAGATTGGT TAATTGAnS	180
AGGCTATGAT GAAGAATTAG GTGCACGTCC ATTAAGACGT ATTGTTGAAC AGCAAGTACG	240
TGACAAAATT ACAGATTACT ATTTAGATCA TACAGACGTT AAACATGTGG ATATAGATGT	300
TGAGGATAAC GAATTAGTCG TAAAAGGTA	329

(2) INFORMATION FOR SEQ ID NO: 4205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4205:

GGTAAACAAA AACTTCCCT TTGGAAGCGA ATTATGGAGC GGAAGATAGG ATTTACACCT	60
ATACCTCGTT CCGGGAAGGG CTGTTTCTAA AAGTTGAACT ACTCCCGCAA ATATTAAATT	120
ATGGAGCGGA AGATAGGATT TACACCTATA CCTCATTCCA GGAAGGAATG TATTCTAAGA	180

GTTGAAATAC TCCCGCATTA TTATTAAATT ATGGÆCGGA AGTAGGATTT GCACCTATAC	240
CTCGTTCCGG GAAGGAGCTG TTTCTAAAAG TTGAACTACT ACCGCATAAA CCTGGTGGCG	300
GCAACCGnAT TTGAACCCGT GATnAAGGTT TTGCAGACCT nTGCCTTTAC CACTTGG	357

(2) INFORMATION FOR SEQ ID NO: 4206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4206:

TACTTTGTGA ATCCAGAAAA CTTTGAGGAT GTCACTAATA GTGTGAATAT TACATCCCA	60
AATCCAAATC AATATAAAGT AGAGTTTAAT ACGCCTGATG ATCAAATTAC AACACCGTAT	120
ATAGTAGTTG TTAATGGTCA TATTGATCCG AATAGCAAAG GTGATTTAGC TTTACGTTCA	180
ACTTTATATG GGTATAACTC GAATATAATT TGGCGCTCTA TGTCATGGGA CAACGAnnAG	240
CATTTAATAA CGGATCAGGT TCTGGTGACG GTATCGATAA ACCAGTTGTT CCTGAACACC	300
TGATGAGCCT GGTGAAATTG AACCAATCCA GGGATCAGAT CTGACCCAGG TCAGATCTGG	360
CAGCGATCTA ATCAGnAGCG GTCAGATCGG GnAGGATCAC	400

(2) INFORMATION FOR SEQ ID NO: 4207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4207:

AAAAAGTTGA GAAAAATGTT TGAATCAGCA ÆCGTTGTGC AATCGAAATT TCCACACCAT	60
CAAAACCTGC TTTAATCGCG CGTAATGTAG CATCGCnGwk ACTGCTGAAT GATGCTATTG	120
ATTTTCTCAT GAGACATGGC GATAACATCG TGTTtCAATC GGTGAATGCA ATGwCATAGG	180
GCTTGGTCCA TACACCTTTC CAAAATTTAA AATGGCTTGA TTTGAAAAAC GACCAGÆTG	240
CGCTACTGGG ATAATAGCGA GGCTACCATG TTGTTTCATC GTAGATCCCA TGTTAGTTAA	300
TCCAGGGATA CAACCATCAT GATCAATATT AAAnCATATC CAACCATTGA CCATAAGGTC	360
AATGTAACAC GCCGGTGACT TCATCCAGCT GAATAGACGC GT	402

(2) INFORMATION FOR SEQ ID NO: 4208:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4208:

```
GAAGAGTTGC AGCAGCAGAT ACAATTTATC CATTCACTCA AGCTGAAAAT GTTTGGTTAC      60
CAAACAAAAA TGACATCATC GAAAAAGCAA AAGAACTTT AGAATTTTAA TACATTTTAA      120
AAGTTAACGA ATTAGCCGTG ATTTTAGTCT CATTGATTAA AATGAAATnG TTAATTTACG      180
AAATCTTAGG AGGGCAAAAA CGTGGGCATT TGATTTAGA TTACCCGATA TCGGGGGAAG      240
GTATCCACGA AGGTGAAATT GTAAAAATGGT TTGTTAAAGC TGGAGGATAC TATnGGAAGA      300
AGACGATGTT TTAGCTGGAG GTACAAAACC GATAAATCAG TAGTAGAAAT CCCCATCCAC      360
CAGCATCTGG TACnGGTAAG                                     380
```

(2) INFORMATION FOR SEQ ID NO: 4209:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4209:

```
AATAAACCTC AGGCTATTCA ATGGCATACA AATTTAACGA ATGAGCGATT CACTACTATC      60
GCACATCGTG GCGCAAGTGG CTATGCACCC GAGCATACGT TTCAAGCATA TGATAAGAGT      120
CATAATGAGT TAAAAGCATC TTATATCGAA ATTGATTTAC AACGTACCAA AGATGGCCAT      180
TTAGTTGCTA TGCATGATGA AACTGTTAAC CGTACAACAA ATGGACACGG TAAAGTTGAG      240
GATTATACCC nTGATGAATT AnAACAGTTA GATGCAGGAA GTTGGTTAAT AAAAAATATC      300
CnAAATACGC CAGAGCAGTA TTAAATGCT AAAGTACCAC TTAGGTGGAA TTTAGGACGT      360
ATTGGCCCGA TGCCAACnTT TATATTGAAC CAAG@CCTG                                     400
```

(2) INFORMATION FOR SEQ ID NO: 4210:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4210:

GCCCACAACC ACAAAGGCTG TAGGCTACAA ATATGGAGAC GCGGGGATTT GAACCCGCGT	60
CCAAAGGTCC TGATACACAT CTTTCTACGT GTGTAGTTTA TCGATAGGTT TCGCATCATG	120
AAAAGTGATA AACAACCAAC ATGATGCTAG TTTGATTAAAG TTTCTTCTAA ACAGATTCA	180
AACGGCATnG TTAGCATATC CTATTAAGGT TGAATCGCGT TAACAGCACA TAGGAAATGC	240
TGTTAGGCGA TGCAGAGTGC GATTAGGCAG CTA CTGCGAA ATTATTGTnT GATTTGCCAG	300
TTATTATnAA CTGTGTGGTG TTGATGACGA	330

(2) INFORMATION FOR SEQ ID NO: 4211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4211:

AAATCATCTT ATGACTGCTT TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC	60
GTTTTCACTT CGCCAAGCCA TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT	120
AAAAAAGAG ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG	180
TTCTACTCTA GCGGAACGTA AGTTCGACTA CATCGACGC TAAGGAGCTT AACTTcnGTG	240
TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC CAGACATATG AATGTAAATT	300
ATACATTCAA AACTAGATAG nAAGTAAAAG TGATTTTGC	339

(2) INFORMATION FOR SEQ ID NO: 4212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4212:

GCGATGGTTG AAACATTGAC TGATATTAAA GAGTTTATGA ACCAAGTTGA TCGCATAGC	60
TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG G TACTACATG	120
CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG	180
CGATTTTGGC ATGAAGGTCA CCTnAAATGT ACATTGTTGT AATAAAATTG CCTATAAAAT	240
TTTTAGCACA TAAAATAAGA GGGGCCAnCC ATTTTAGACT ATAACAACGG TTGGCTCTTT	300
GAATTGTAAA AAGAAAACCA TACGCTATGn TATT	334

(2) INFORMATION FOR SEQ ID NO: 4213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4213:

```
CTATGATTTC ACCGAGTCTC TCGTTGAGAC AGTGCCCAA TCGTTACGCC TTTCGTGCGG      60
GTCGTTACCC GACAAGGAAT TTCGCTACT TAGGACCGTT ATAGTTACGC CGCCGTTTAC      120
TGGGGCTTCG ATTCGTAGCT TCGCAGAGTA nACCCACTCC TCTTAACCTT CCAGCACCGG      180
GCAGGCGTCA CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAACA      240
GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGGCGTTA ACCCTAAAGA GCACCCTTC      300
TnCCGAAGTT TACGGGGTCA nTTTGCCGAG TT      332
```

(2) INFORMATION FOR SEQ ID NO: 4214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4214:

```
CGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTGGCT ACCATCGTCG CTAAAGACCT      60
TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTAATCATTT      120
AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC      180
GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TAnTTTGACG TTTTAGACAT AAAAAAAGA      240
GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGGCAA CGTTCTACTC      300
TAGCGGAACG TAAGTTGGGT ACCATCGACG CTAAGAACCT TCTTGGAnTG TGGACAACGn      360
TGG      363
```

(2) INFORMATION FOR SEQ ID NO: 4215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4215:

ACTCATCATT ACAATTTGGA CATAAGTCT ATTAAAnCGT GTGCCATTTG GAGTCCACTT	60
TTATTTGTAT TGTATAGAGA GAAATAAAAA GAnACCTTGT TTTACAAGGTTTCTAATACG	120
TTATGTTATG TAAATAACAG TTAATTATAC CGGTGGTCGG GGTGGAACCG AACTCCACA	180
AGTGGAACGG GGATTTTGAG TCCCGCGCGT CTGCCAATTC CGCCACACCG GCTTAATGGT	240
AAACAAAAAA CTTCCCTTTG GAAGCAATTA TGGAGCGGAA GATAGGATTT ACACCTATAC	300
CTCGTTCCGG GAAGGACGTG TTCTAAAAGT TGAATACC	338

(2) INFORMATION FOR SEQ ID NO: 4216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4216:

ACGGTGATCC CATAATGCTT GAACATCAAT TTCATCCATT AATGTTACAT GAGGTGCAGT	60
ATGCTTAGAG TTAACCATTG CTTTCGCAAT TGCTCTACGC ATAGCAGGGA TTTTTTCAGT	120
TGTTTCTGGG AAGTCGCCTT CTAATGTTAC TGCTGCAGGT GCTGCAGGAG TTTCAGCAAC	180
TTCTTCACTT GTAGCTGAAG CAGCTGATTC ATTTGAAGCT GTTGGTGCAC CACCATTTAA	240
GTATGCATCT ACATCTTCTT TTGTAATACG ACCATTTTTTA CCAGATCCAG AAAGTCTTTT	300
AATGnTAACA CCTnTTTCAC GTGCGTATTA CGACTGAAGG CATGCCTTAA AGTCnGGTT	360
CACCACTCTC AGTTGAGAGC ACAGGGCTGC nCGCTGGCGC	400

(2) INFORMATION FOR SEQ ID NO: 4217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4217:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT	60
GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC	120
CCCATTCCGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA	180
GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA	240
TCTATGTTTC CATCCTACAG GAAACGCGTT ATTAATCTTG TGAGTGnCT TTCGAACATA	300

GGCGGATTAT TTCTnATGAA TTCAAGCTA TGTGAAAACT CnTTA

345

(2) INFORMATION FOR SEQ ID NO: 4218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4218:

GGCGCCCTCG TGCCAAACAG TGCTCTACCT CCAATAATCA TCACTTGAnG CTAGCCCTAA	60
AGCTATTTTCG GAGAGAACCA GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA	120
GTTTCATCCGC TCACTTTTCA ACGTAATCGG TTCGGTCTC CAnTCAGGT TACCTGAACT	180
TCAACCTGGA CCAAGGGTAG ATCACCTGn TTCGGGTCTA CGACCAAATA CTAAACGCCC	240
TATTCAGACT CGCTTTCGCT GACGGCTCCA CATTTACTGC TTAACCTTGC ATCAAATCGT	300
AACTCGCCGG TTGCATTCTA CAAAAGGCAC GCCATGCACC CATTA	345

(2) INFORMATION FOR SEQ ID NO: 4219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4219:

TCTTATGACT GCTTTTTATT ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTTC	60
ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA	120
AGAGACCTTG CGGTCTCAAT GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC	180
TCTAGCGGAA CGTAAAGTTC GnACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTCG	240
GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGGAAT GTAAATTATA	300
CATTCAAAAC TAGATAGTAA GTAAAGTGGn TTTGCTTCGC AAACnTTAT TTTGGTTAGT	360
CTTCGTC	367

(2) INFORMATION FOR SEQ ID NO: 4220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4220:

AAGAGCCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCACTT	60
ACTCATTTAG CTCTACTAAA CTCGTTGCGT TCTTTTCTCG TTTCGTCAGA TTCAAACGTT	120
TTCACCTTCGC CAAGCCATTT TTCTTTGTGT TTGCTTTTTTA TTTTGACGTT TTAGACATAA	180
nAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT	240
TCACTCTAGC GGAAnTAAGT CGAACTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGTT	300
CGGCATGGGA ACAGGTGTGA CCCCnTGGC TATAGTCACC AG	342

(2) INFORMATION FOR SEQ ID NO: 4221:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4221:

ACCGGATGAC AGCCCCAGGA TGCGATGAGC CGACATCGAG GTGCCAAACC TCCCCGTCGA	60
TGTGAACTCT TGGGGGAGAT AAGCtGTTAT CCCCGGGGTA GCTTTTATCC gTTGAGCGAT	120
GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT	180
AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGÆTTC CAACCATTCT	240
GAGGGAACCT TTTGAGCGCC TCCGTTACCT TTTAnGAGGC GACCGCCCCA GTCAAACCTGC	300
CCGCCTGACA CTGTCTCnCA CCACGATAAG TGGCGnG	337

(2) INFORMATION FOR SEQ ID NO: 4222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4222:

GGCGCTTGAC TAAAAAGAAA TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT	60
TTACCAAGCA AAACCGAGTG AATAAAGAGT TTTAAATAAG CTTGAATTCA TAAGAAATAA	120
TCGCTAGTGT TCGAAAGACA TCCACCAAGn TTAATAACGC GTTTAAATCT TTTTATAAAA	180
GAAACGTTT AGCAGACAAT GAGTTAAATT ATTTTAAAGC AGAGTTTACT TATGTAAATG	240
AGCATTTTAAA ATAATGAAAA CGAGCCGTAT GTGAGCGTTT GACTTATAAA AATGGTGnA	300

ACATAGATTA AGTTATTAAG GGCGCACGGT GGGTGCCnTG GCACTTAGAA GCCGCTGAAG 360
G 361

(2) INFORMATION FOR SEQ ID NO: 4223:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4223:

CGGTAGAATA CAACCTTGCC AAGGTTGGCG TCGCGGGTTC GATCCCGTC TTCTGCTCCA 60
 TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC TTAAAATCCT GCGGTGAGAG 120
 ATCACCGTAC CGGTTGATT CCGGTCCTCG GCACCATTTT AGCGCCCGTA GCTCAATTGG 180
 ATAGAGCGTT TGACTACGGA TCAAGAGGTT ATGGGTTCTGA CTCCTATCGG GCGCGCCATT 240
 TTTAAATTAA TTGAATAACG GGAAGTTAGC TCAGCTTGGT AGAGCACTTG GTTTGGGGAC 300
 CAAGGGTCGC AGTTCGAATC CTGTCTTCCC GATTACTCnT AAnTCCATTT AnGGGGGCTA 360
 GCTCAGTGGG GAGAGCGCTG CTTGCACGCA GGAGGTCACG 400

(2) INFORMATION FOR SEQ ID NO: 4224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4224:

CATAATATAC TCTTAAGTGT AAAGGGGAAT TTCCTGGGTA ATAATTCGCG TGTGCACCTT 60
 GAGTGACTTC TACCATTTTA TAGTCAAATT GCTTTAGTTC GTTTGGTTTA ACGCCGACAC 120
 TCGCAAATGT ATAATCAAAG AACTTCACAA TATTGTTGCC TAAGAAGCCT TTGAATTCAA 180
 TAGTGTCATT TCCAGCAATT TGTTGGGCAA CAATACTTGC TGCGGGGTG AGCGCCCCCA 240
 GnCAAAAGGA CCACTAGCCG GTAGAATCGA CATGTCGATA ATGTGATGGT TGCCAATAAT 300
 CGCCTATTGC ATAATGTTTG GACCATTGGT TCCAAATTTA TCGTTACCGG TATGAAACCT 360
 TTCGATCCAG TTGGATAATT GAACTTCGnA AATTTGATTG 400

(2) INFORMATION FOR SEQ ID NO: 4225:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

GGGTTCAATT TCTGCATACC AATCGATGCC AGCTCTATTT CTGACAATAT CCATATATTT	60
TGAAATTTTC TCTAATTCTT TGCCACTAAC CTTTTCACCA TTCAACCAAA ATTGATCCTG	120
TGTTAACTGG TCGTTAAAAG TGACTTTCGT TTCAGTGTA AATTTTCTA ATGTAACAGA	180
TATGCTATTA TTCATTGGAA TGATTAGTGC TTCATCTTTT TTACCCCAAT ATTTTATnAG	240
TGCAATATTC GTATGTGCAC GTGCTTTGCC ACTnnTAATC AACGCATTAA CTCCTAAAT	300
TCTCAATCCA AGTATGTGCT GCACCAGC	328

(2) INFORMATION FOR SEQ ID NO: 4226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4226:

TGACGGGTTT GAACCGCCGA CCCTCTGCTT GTAAGGCAGATGCTCTCCCA GCTGAGCTAA	60
TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC GGAAAnGTAAG TTCGnACTAC	120
CATCGACGCT AAGGAGCTTA ACTnCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC	180
TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT	240
GATTTTGTCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC	300
TCCACATGTC ACCATGCTTC CACCT	325

(2) INFORMATION FOR SEQ ID NO: 4227:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4227:

GCGCAACTCA CACAACAAGG TGGCAATCAC TCTGAACAAA GTGCGGCAAn TnTTCAACA	60
AGCAGCACAC AACAAAGGCA ACAAGGTGGC AACGGCAATT ATTTAGAACA AATTGGTCGT	120
AACCTTACGC AAGAAGCACG TGACGGTTTA TTAGATCCAG TCATTGGTCG TGGATAAAGA	180

AATTCAAGnA ACTGCTGAAG TTTTAAGTAG' ACGAACTAAA AACAATCCTA TATTAGTTGG	240
AGAAGCTGGT GTTGGTAAAA CTGCGATTGT TGGAAGGTTT AGACAGGCA ATCGTTGGAA	300
GGAAATGTAC CAGCAGCAAT CAAAGACAAA G	331

(2) INFORMATION FOR SEQ ID NO: 4228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4228:

AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCATTAATA ATAAGGGCGG CTGAAGGGGA	60
TCGAACCCTC GAATGTCGGA ACCACAATCC GATGTGTTAA CnCTTCACCA CAGCCGCCAT	120
GGCAGGGGCA GTAGGAATCG AACCCACACC AAAGTTTTGG AGACCTCTAT TCTACCGTTG	180
AACTATGCCC CTATTAAAA TAATAAATGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA	240
AGAGCGGATT TACAGTCCGC CGCGTTTAnC CACTTCGCTA CCCCTCCATA AATGGTGCCG	300
GCCAGAGGAC TTGnAACCC CAACCTAATG GTT	333

(2) INFORMATION FOR SEQ ID NO: 4229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4229:

CTCTTACTTT GTAAACCAAA TCTTAAATTA AAATATTGAA AATGCAATGn ATCCTTAATA	60
TTTTATTAAA CCTATAATTA CTTATTAAAA ATAACACACA ATATTCATAA AGTTTTAAAA	120
ATATTCTGTT TTATCACCTA CTATTAGTGG AAAAGTACA TTGCAATTGT ATATAGTTTG	180
CATAACGCTT CAAAAGTAAT TTCTTTTTTG TTTAGTTCAA AAAAAATTTAG AGGTGATGTT	240
ATATGAATAA CGGTTTTTTC AATAGCGACT TTGATTCAAT TTTTCGAGGA TGATGAAAGA	300
TATGCAAGGT TCAAATCAAG TCGGAAACAA AAGTACTATA TTnATGGTAA GGAGTTTCAC	360
CTGAGGACTG GCGCAACTnC ACACACCAGG TGGCCATCAC	400

(2) INFORMATION FOR SEQ ID NO: 4230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4230:

```
CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTT ACTCCCCCTT      60
CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGTTCAC TATCGGTCAC AGAGAGTATT      120
TAGCCTTAGG AGATGGTCCT CCCAGATTCC GACGGAATTT CACGTGCTCC GTCGTA CTCA      180
GGATCCACTC AAGAGAGACA ACATTTTCGA CTACAGGATT ATTACCTTCT TTGATTTCATC      240
TTTcCAGATG ATTCGTCTAA TGTCGTCCTT TGTAAC TCCG TATAGAGTGT CCTAsAACCC      300
CAACAAGCAA GCTTGTTGGT TTGGGnTCTT GCCGTTTCG      339
```

(2) INFORMATION FOR SEQ ID NO: 4231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4231:

```
GAAGTCATAT GCATACACTT GGTTATCATT ATTCATACGT TCAATCGCAT CTGTAACTG      60
AATTTTCGTTA CCTGCGCCTT CTTTTTGC GT TTTTAAATAA TCGAAAATTT CAGGCGTTAA      120
TACATAACGT CCCATAATAG CTAGGnTTGA TGGTGCCGTA CCTTGTGCTG GCTTTTCAAC      180
AAACTTTTTT ACTTCAGACT GACGTCCGTn TTTAGTTAAT GGGTCAATAA TTCCATAACG      240
ATGAGTATCT GCTTCCGGAA CTCTTGGAC ACCTATAACT GAGTGCCCTG TnTCTTCATA      300
AACGTCAATC AACTGTTTCA CTGCTGGCAC TTCAGAGTCA ACAATATCG      349
```

(2) INFORMATION FOR SEQ ID NO: 4232:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4232:

```
CCCAGCTCGC GIACCGCTTT AATGGGCGAA CAGCAAGCGC CTGTGGGAnC GACTACAGCC      60
CCAGGATGCG ATGACCGACA TCGAkGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG      120
GAGATAAGCC TGTATCCCC GGGGTAGCTT TTATCCGTTG aGCGATGGCC CTTCCATGCG      180
```

GAACCACCGG ATCACTAAGT CCGTCTTTCG ACCCTGTCG ACTTG TAGGT CTCGCAkTCA	240
AGCTCCCTTA TGcCTTTACA CTCTATGAAT GATTTC AAC CATTCTGAGG GAACTTTGaG	300
CGCCTCCGTT ACCTTTTAGG AGGCGACCGC CCAGTCAAAC TGCCCGCCTG AACTGTCTC	360
CCACCACGAT AAGGTCG	377

(2) INFORMATION FOR SEQ ID NO: 4233:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4233:

GGCTAGCCTC AAGTGATGAT TATTGGAGGT AGAGCACTGT TTGGACGAAG GGCCCCTCTC	60
GGGTACC GA AGTTCAGACA AACTCCGAAT GCCAATTAAG TTAACTTGG GAGTCAGAAC	120
ATGGGTGATA AGGTCCGTGT TCGAAAGGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA	180
AATATATGTT AAGTGGAAAA GGATGTGGCG TGGCCCAGAC AACTAGGATG TTGGCTTAGG	240
AAGCAGCCGT CATTAnAGA GTGCGTAATA GCGCACTAGT CGAGTGACAC TGGGGGGAAA	300
GGGTACCGGG GCTGAACATA TTACCGAAGC TGGTGGGTTG TCCTTTGGAC AnTTn	355

(2) INFORMATION FOR SEQ ID NO: 4234:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4234:

ATCCGCCTCC CGCAATATTT TATAGGTCTC GT AT GTAGC GnTTAACACG CCTGCCTGTC	60
ACGCAGAGAT CGCGGGTTCG ATTCCCGTCG AGACCGCCAT CATTACATTT TTATTATGGT	120
TCAGTAGCTC AGTTGGTAGA GCAATGGATT GAAGCTCCAT GTGTCGGCAG TTCGACTCTG	180
TCCTGAACCA TTTCTTAGCC GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCA E	240
AGGTTGGGGG TTCAAGTCCT CTGGCCGGCA CCATTTATGG AGGGGTAACG AnTGGGCTAA	300
ACGCGGCGGA CTGTAAATCC GCTCCTTCGG GGTTCGGCAG TTCGAATCTG CCCCCTCCAA	360
TTAATAATTT TAATAAGGGG CATAnTTCAA CGGTAnAATA	400

(2) INFORMATION FOR SEQ ID NO: 4235:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4235:

```

ATGCCATGTT CACCTTGTTT AAAATCAAGG TTTGTAATGT TTCCTTGTGT CACGATAATA      60
GGCGTAATAT CACTCTTTGC ATGATTGCGG ATGTAGTCTA AATCAAAGTT GATTAATAAA      120
TCACCTTCTT TAACTnnTTG ACCTTCCTCA ACATGTAAAG TAAAGCCTTC TCCGTTTAAT      180
TTAACAGTGT CTAAACCGAT GTGGATTAAT AGTTTAAAC CACTATCTGA TACAAGACCA      240
ATTGCATGnT TTGTTGGGAA AATCATTTGT ACTTTACCGT TGAATGGTGC ACGAACTTCA      300
CCTTGTGAGG TTTGATAGCG ATACCGTCAC CCATGCATTT T                          341

```

(2) INFORMATION FOR SEQ ID NO: 4236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4236:

```

GTTGATGCAG CCCGTTGAGC TCTAAACCAA CTGAGCTAAA GGTCCTAAAT ATAATTTAC      60
AACTAATAAA TAGTGGCGGT GGAGGGGATC GAACCCCGA CCTCACGGGT ATGAACCGTA      120
CGCTCTAGCC AGCTGAGCTA CACCGCCTTA TATAGTTTGT AAATAATATG GTGGAGACTA      180
GCGGGATCGA ACCGCTGGAC CTCCTGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAG      240
CCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCG AACCTGCGAC CCCTTGGTCC      300
CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGnGC CCGTAGGAGT      360
TGAACCCATG AACCTnTTGA TCCnTAGTnC AAACGGTCTA                          400

```

(2) INFORMATION FOR SEQ ID NO: 4237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4237:

```

nAnTTCTTGA CCTGACATCA CCTGAAATTG ATGGACATG GTCCACCAGG TCATATACTC      60

```


TAATCCATGG GTCGCCGATA CCTTCAACGn ACAACATCTA CACCACTATT TCTAATACAG	120
AATCTTTCTC CTGCACTACC GTTAATAAAT GCCTTACCAC TTGTCGCACC ATAGAATGAG	180
ACGTTACCAG CAATAATTTT ATTTTGTCTG TCTTCAAAAG GTGCTTTGAC AATGAOGTA	240
CCACCAGATA ATCCTTTACC AACATAGTCA TTCGCATCTC CAGTATGATG AATCATTAAG	300
CCTTTCGGTG CATATGCTGC AAGACTTTGA CCAGCATGAC CATTCGTATA AACATTAATT	360
GTATTTTCAG GAAGTC	376

(2) INFORMATION FOR SEQ ID NO: 4238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4238:

CGATTTAAAG CTAAGCCCAT TTTCGCTCTT TCTCCATAGC CTAACCAAGC AATACGTGAT	60
GGTAGTCCTT GATATGAAAT TTTTCTTCA GCTAAATCAA GCCATCTTAA TAACTTTTCA	120
TTTTCTGGGA AAAGTTTGCG CATTTCTTCA TCCGCACGCT CGATATCTTT TGGATCACCA	180
CTCAACGCAG CAAAGCGGAA TGGCCCTTTA CCTCACAGA ATAATGGTCT AATGTAAGCT	240
GGTACAAAAG CTGGGAAGTC AnAAAGCATT TTTCCTCCG TATTGAAGGC TACTTGACGA	300
TATGnTACCA TAATCAATGC TACAGCGCCA CGTTG	335

(2) INFORMATION FOR SEQ ID NO: 4239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4239:

CCACAnTTAC AAGCAACTAC TGAAGGCGCT GTATTTATTA AAGGTGGCGA CGETTTGAT	60
TTCGGACACG TAGAAAGATT TATTCAAAAC CCGCCACATG GGGCAACGGT TGCATGGCAT	120
GATAGTCCAG ATACATGGAA GAATACAGTC GGTAACACTC ATAAAACTGC GGTTGTAACA	180
TTACCTAATG GTCAAGGTAC GCGTAATGTT GAAGTTCCAG TCAAAGTTTA TCCAGTTGCT	240
AATGCAAAGG CGCCATCACG TGATGTGAAA GGTCAAATTT TGCTGTTGGA CGGATGCGAT	300
GAACTACATT ACATTTGTCC AnTACAACAC AGATnGTATC ACTGCAGC	348

(2) INFORMATION FOR SEQ ID NO: 4240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4240:

TTGATGTTAA AGATTTAGCA AGGGGCGAGA GAACTGGAGA AGAGGTTGCC AAACGAATGG	60
AACGTGCTTC TGTATTGGCC CAAGTAGATA TTCATCGTGC AGCAACACAT AATAAAGGTG	120
TTATGAATGG CATACTGCT GTTGTTTTAG CAACAGGAAA TGATACGCGT GGTGCAGAAG	180
CAAGTGCGCA TGCATTACGC GAGTTCGTGA CGGACAGTAT CGTGGTATTG CTACATGGCG	240
TTACGATCAA GATCGTTCAA CGATTTGATT GGTACATTGG AAGTGCCTAT GACATGGCA	300
ATCGTTGGCG GTGGGTACAA AAGTATTACC AATTGCTAAG CCTTCATTAG GAGnTACTAA	360
ATGGTAGAGT CCGCCCCAAG AATTAnGnCC CTGTA	395

(2) INFORMATION FOR SEQ ID NO: 4241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4241:

ACTAATGATT TATTATGTAG TGGTTCTTTG TCATTAGCCA CAGCTATTGT GTACTTAAAA	60
ATAGGAATGC ATGAGTGCAA CTCTAnAnGn AGCATACTAA TTTCTAAAGA AAAAGTATTT	120
CTTTATGTTG GGGCCCCGCC AACTTGCATT GTTTGTAGAA TTTCTTTTCG AAATTCTTTA	180
TGTTGGGGCC CCGCCAACTT GCATTGTTTG TAGAATTTCT TTTGAAATT CTTTATGTTG	240
GGGCCCCGCC AACTAATTCC AATATATCAT TTAGAGCTT AGGTCATTGA TTTTGGCTC	300
GGACTTTTAT GGCGATATGA ACCATGTAAA T	331

(2) INFORMATION FOR SEQ ID NO: 4242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4242:

TGCATTGCAT TATTGTACTG CGTAATTGTA CCTGGCTTTT TACCTTCAGT GCTTACTGGA	60
TCATCTAAAT GATTTTTAGC TGTGATTAAC TCACGTTTAT CCGCTTTTGT AAA ATGGAC	120
TCTTGACTT CTTCAGTACT ACCATCATTG TAAGTTACTG TCACAGGAAT CGTCGTTGTG	180
CTACCACCAG CTAAATTAGT AGGCATTGCT GTGCCATTTT TAATCGTTGC AGTACGTTTA	240
TTAGCAACTT GAACTGCATT GTTAATTTCA GCTGCTGTTA CATTGAACC ATAATCTTTC	300
ACAATTnCAG TTGTGTTGAC AGATGAGnGG CGGTGCAGTA AGGACTGGAT AACTACGAG	360
TGACCGGACT GCTTCGGGnA ATGTGATGA	389

(2) INFORMATION FOR SEQ ID NO: 4243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4243:

ATACGCATGT TAACGATCGA ATGCTTAATG TCCCGGGAAA TAAATCTATC ATAAGTTACT	60
TTAATGAAGT TGTCTCACGA CAAGGTAATC ATGTTGCGCT ATCATGAATG ATTTGACAAT	120
GACGTATGAA CATTACGCAA CTATGTGGAT GCCATTGCGC ACATGCTCCT ATCAAATGGT	180
GTGGGCAATG GTCAACGGGT TGCCTTGTTT ACAGAACGTn TTTTGAAAT GATTGCGGCG	240
ATGTTGGCGA CAGTTAAAGT AGGTGCATCT TATATACCTA TCGATATTGA TTTCCGAAT	300
AAACGACAAG GTGCAATTTT GG	322

(2) INFORMATION FOR SEQ ID NO: 4244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4244:

GCCGACTACT GAAGGGnAAT CGnAATTTTC TTTCTCTTCC TCCGGGGGAC TAAGATGTTT	60
CAGTTCTCCG GGTGTGCCTT CTGTATATGC TATGTATTCA CATATCGATA ACATGACATA	120
ACTCATGCTG GGTTTCCCCA TTCGGAAATC TCTGGATCAA AGCTTACTTA CAGCTCCCCA	180
AAGCATATCG TCGTTAGTAA CGTCCTTCAT TGGCTTCTAG TGCCAAGGCA TCCACCGTGC	240
GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATAA GTCAAACGTT AACATGAAGT	300
TACGTTCTTT TATAAAAAGA TTAAACGCG TTATTAATC	339

(2) INFORMATION FOR SEQ ID NO: 4245:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4245:

CCATTAACGG GCTCTGACTA CTTGTAAGCA CACGGTTTCA GGTTCATTT CACTCCCCTT	60
CCGGGGTGCT TTTCACCTTT CCCTCACGGT ACTGGTTCAC TATCGGTCAC TAGAGAGTAT	120
TTAGCCTTAC GAGATGGTCC TCCCAGATTC CGACGGAATT TCACGTGCTCCGTCGTACTC	180
AGGATCCACT CAAGACAGAC AACATTTTCG ACTACAGGGA TTATTACCTT CTTTGGATTC	240
ATCTTTCCAG ATGATTGCTC TAATGTCGTC CTTTGTAACCT CCGTATAGAG TGTCCTACAA	300
CCCCAACAAAG CAAGCTTGTT GGTnTTGGGC nACTTCCCCG TTTCGGTTCG GCCGCnAA	358

(2) INFORMATION FOR SEQ ID NO: 4246:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4246:

AAAGAGACCT TGCGGTTAGA TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAACGTTCTA	60
CTCTAGCGGA ACGTAAGTnG AnCTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG	120
CATGGGAACA GGTGTGACCT CTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA	180
TTCAAAACTA GATAGTAAGT AAAAGTATT TTGCTTCGCA AAACATTTAT TTTGATTAAG	240
TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGGAACCTA	300
TTAACCTCAT GCATCTTTGA GGGGnGCTTG ATAACCGA	338

(2) INFORMATION FOR SEQ ID NO: 4247:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4247:

CCCCGGGTAG CTTTTATCCG TTGAGCGATG GCCCTTCCAT GCGGAECAC CGGATCACTA	60
AGTCCGTCTT TCGACCCTGC TCGACTTGTA GGTCTCGCAG TCAAGCTCCC TTATGCCTTT	120
ACACTCTATG AATGATTTCC AACCATTCTG AGGGAACTTT GAGCGCCTCC GTTACCTTTT	180
AGGAGGCGAC CGCCCAGTCA AACTGCCCCG CTGACACTGT CTCCCACCAC GATAAnGGCG	240
GGGGTTAGAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCTCCACG TAACTAnCGC	300
TCACGTTTCA AAGnTCTACC TATCCTGTAC A	331

(2) INFORMATION FOR SEQ ID NO: 4248:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4248:

ATAATCATAC AGATGGCAAT ACAACAGCAA CTGAGACAGT GTCAAACGCT AATAATAATG	60
ATGTAGTGTC GAATAATACC GATTAAATG TACCAACTAA AACAAATGAA AATGGTTCAG	120
GAGGACATCT AACTTTAAAG GAAATTCAAG AAGATGTTCG TCATTCTTCA AATAAACCAG	180
AGCTAGTTGC AATTGCTGAA CCAGCATGCT AATAGACCGA AAAAGAGAAG TAGACGTGCG	240
GCACCGGCAG ATnCTTAAAT GCAACTTCCA GCCAGATCCA GCGGCTGEG CGGTAnGGAA	300
ACGGTGGTGC CACCAGTTTG CCAATTTACA GCGCCCATAT TACGCCAACA ACTGGTnCCC	360
TAATGCCCAA T	371

(2) INFORMATION FOR SEQ ID NO: 4249:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4249:

AATTGCATGG CATAACATCG GCGATTAAAA GATGGACGTT TTGATGATGT ACAACAAGAC	60
ATTGAAGCAG TGGTGAAAGC TGCGAAGGTC ACACAGTAAA AGTGATTATT GAGACGGTAT	120
TGTTGGACCA TGACGAAATT GTAAAAGCGA GTGAATTAAC AAAAGCGGCT GGTGCGGACT	180
TCGTTAAAC TTCAACAGGT TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAATTAAT	240
GAAAGATACA GTAGGTGCTG ATATAGAAGT AAAAGCTCAG GTGGCGTACG TATTnTAGAA	300
GTTTCAATGA AnGGTTGAAG CAGGTGCGAC ACGTAnTGGT GCGAGCGCAG CGTTCAA	357

(2) INFORMATION FOR SEQ ID NO: 4250:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4250:

```
GAGCCCAAAC CAACAAGCTT GCTTGTTGGG nGTTGTAGGA CACTCTATAC GGAGTTACAA      60
AGGACGACAT TAGACGAATC ATCTGGAAAG ATGAATCAAA GAAGTAATA ATCCTGTAGT      120
CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAACACGTGA AATTCCGTCG      180
GAATCTGGGA GGACCATCTC CTAAGGCTGA ATACTCTCTA GTGACCGATA GTGAAGnAGT      240
ACCGTGAGGG AAAGGTGAAA AGCACCCCGG GAAGGGGAAG TGAAATAGAA GCTGGAAACC      300
GGTGTGCTTA CAAGGTAGTC AnAGCCCGTT AATGGGTGAT GCGTGCCTT TT              352
```

(2) INFORMATION FOR SEQ ID NO: 4251:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4251:

```
CATTTACTGC TTAACCTTGC ATCAAnATCGT AACTCGCCGG TTCATTCTAC AAAAGGCACG      60
CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTTAC      120
TCCCCTTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG      180
AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT      240
CGTACTCAGG ATCCACTCAA GAGAGACAAC ATnTTCGACT ACAGGATTAT TACCTTCTTT      300
GATTCAAnCTT TCCAGAATGA TTCGTCTAAT G                                  331
```

(2) INFORMATION FOR SEQ ID NO: 4252:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4252:

TATTTGATAT TTTGTGCATT GCAGTCAAAC CATGGCGGAA ATTGAACCAA TACCATTGCT	60
AATTTTTTCT GTGTATGTAA GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTnGC	120
CTTGTATCTG CAAATGTTTT GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC	80
ACAAATTCAA ATGTATCAGG CGTTTCTTTT ATCCATTTCA ATATATTTCT TTCCGGTTGT	240
ATCGCATAGT ATGTCGCATC TAATTCGCAA CCGGAAAATG TCCAGCATAT GTTTTAAGGT	300
TATCGGTTTG GCGTTCTAAA TCTGCATATA ATGAATAGTG ATCACCCCAA CCTGTTAAAT	360
CCGATGGTTA TCCAnATGAT GATCACCATG TCATCAnACC	400

(2) INFORMATION FOR SEQ ID NO: 4253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4253:

AAAGGTATCA AAGATGTTAA AGTTACTTTA TTAAATGAAA AAGGCGAAGT AATTGGnACA	60
ACTAAAACAG ATGAAAATGG TAAATACTGC TTTGATAATT TAGATAGCGG TAAATACAAA	120
GTTATTTTTG AnAAGCCTGC TGGCTTAAAC ACAAACAGTT A AA AATACAA CTGAAGATGA	180
TAAAGATGCA GATGGTGGCG AGTTGACGTA ACAATTACGG ATCATGATGA TTTCACACTT	240
GATAACGGAT ACTTCGAGGG GATGACATCA GACAGCGATT CAGACTCCAG ATAGTGACTC	300
AGnCAGCGAC TCAGACTTCA GACAGCG	327

(2) INFORMATION FOR SEQ ID NO: 4254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4254:

AGATGACATT AAATAGCATC TCCTCGTGTT GATTATTTTG GTTGGCTGAC CAATATTTAT	60
TCTAGCACGT AGAGATGCAT TTTTGTGAC AATGGTAGAA CCTTTTCTGA ACCATACGCA	120
TAGGATTGTn CTnTTTTACA ATTAAAGAGC CAACCGTTGT TATAGTCTAA CAATGGTTGC	180
CCTCTTATTT TATGTGGCTA AAAATTTATA GGCAATTTTA TTACAACAAT GTACATTTAA	240
GGTGACCTTC ATGCCAAAAT CGCATCACTC ATTTAATGGA AGCAGCACGT CTTCATATAA	300
AGTACCGATC CCTAATTCCA ACGCATGTnG	330

(2) INFORMATION FOR SEQ ID NO: 4255:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4255:

ATTAGTGATT GTAAAAAGT AAAACTATTC TTGGGAGTG GACATAAATC AATGTCTAGA	60
CTCTATAGTG TTGTATTTGG CAGTAGTTGA CGGGGCCCCA ACATAAAGAA ATACTTTTTC	120
TTTAGAAATT AGTATTTCTT ATACATGAGT TTTACTCAGG ATATCCTATT TTAAATACA	180
CATTAGCTGT GTTTAATGAT AAAGAACCAC TACATCATAA ATCTTTAATG GTTCTTTATC	240
AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTAAATCAA TATAATTCAA AAAAGGGTCG	300
AAGATATGAn ATCACATCTT CGACCCThn TTGTACTAAT TTAA	344

(2) INFORMATION FOR SEQ ID NO: 4256:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4256:

CCAGTAATAT CTAAATGAGT TGGATATTTA ACTTTCGCAT TAATTTCAAT ATTAAATTGC	60
GTTACCGCGA CAAGnCATnA CACAACATAC ATAATAAGAT TGGCTAAAAA GATATAGTTA	120
AAGCTAAATT CTGCGACAAA GCCGCCATT GCAGCACCGA CAGCCACACC AATATTTTGC	180
GCTAAGTATA TCGCATTAAA CGTTTGTCTT CCGCCATTTG GCCACACTGC TCCAGCCATA	240
GCGTATATCG CAGGAATAAT CATTCCGCCA CCAAACCCTAACATTACAAG CCATACAGCA	300
TACCAAGGCC ACCCGTGGAn AGA	323

(2) INFORMATION FOR SEQ ID NO: 4257:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4257:

GCTGACTTTC CACCAGCCTC TGTGTTGGGG CCCCGACTAT TTTTGAAAAG AGCGTGTTAC	60
ACGGTCATTG TTTTACAGTC AACTACTGCT AAAATAAAAT TAACGAGCTT AGGGCTTTGT	120
TTTCTGTCCC AAGCTCGTTA AATCACATAT GATAATTAAT TATGCCCAAC CACGATATCT	180
AGCTGCTTCT GCTGTACGTT TAATACCTAT GGATATATGC TGCAnTCTGC ATATCTATTT	240
TTCGGTTTTG AGACAATTCTG TAAATCGTAT CAAATGCCGC TTCTAATTTT TnCACGTGGC	300
TTTTGCATTG AACTTCTTCT nGCAGGACCA ATAATAACCT TGGATTATTT TGTGACCCAT	360
CGGGAGTGA	369

(2) INFORMATION FOR SEQ ID NO: 4258:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4258:

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT	60
TTTTTAAATA CTAAAATACA TGTGGAATA CTTGTCCAT AGAAAATATT GGCTGGTAAC	120
CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGAAT CACACCTTCT	180
GCGGCACCAC GAATAATACA CCATGnGGAG TACGACGCCA nGTACCTTCA TCGTCTAGTA	240
ATGTACCAGT GTTGAATAAA GCAAAGTCTG CTTTGATTTT GGCGCAACTT GCCGTAACCA	300
CTGAATCGTT CATCATTTCA AATTTGAACT GCTGT	335

(2) INFORMATION FOR SEQ ID NO: 4259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4259:

ATTTTCGCTAC CTTACGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTTCGTA	60
GCTTCGCAGC nACAACCACT CCTCTTAACC TTCCAGCACC GGGCAGGCGT CACCCTATAC	120
ATCACCTTAC GGTTTAGCAG AGACCTGTGT TTTTGATAAA CAGTCGCTTG GGCCTATTCA	180
CTGCGnTCT TCTGGGCGTT AACCTAAAG AGCACCCCTT CTCCCGAAGT TACGGGGTCA	240
TTTTGCCGAG TTCCTTAACG AGAGTTCGCT CGCTCACCTT AGAnTTCTCA TCTTGACTAC	300
CTGTGTCGGT TTGCGGTACG GGCA	324

(2) INFORMATION FOR SEQ ID NO: 4260:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4260:

```
AAGCGGTTGT TAGACAATGC ATTAAGAAAA ATTAAAGCGG AGTTTACTTT TGTAATGAG      60
CATTTGATTT TTTGAAAATA AAGCAGTATC GGGCGCTTGA CTAAAAAGAA ATTGTACATT      120
GAAAACTAGA TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGA      180
TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ACGAGCAAGA      240
TTAATAACGC GTTTAAATCT TTTTATAAAA GAAAACGTTT AGCAGACAAT GAGTTAAntT      300
ATTTTAAAGC AGAGTTTACT TATGTnAATG GAGCATTGAA AATnATGAAA ACGAGCCCGT      360
ATGTGGAGCG TTTGACTTA TAAAATGGT GGGAAACATA      400
```

(2) INFORMATION FOR SEQ ID NO: 4261:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4261:

```
AATTAATGTG CGAGTTGGGG TGGGACGACG ATAAAGAAAT ACTTTTCTA TAGAAATTAG      60
TATTTCTTAT GCATGAGTTT TACTCAGTAA TTCCTATTTT TAAGnACACA TTAGCTGTGG      120
CTAAntAGAG GAnACCACTA CATAATAAAT CATTtTGGC TCTTTATCAT TTCTGTCCCA      180
CTCCCCTGAG AAGTTTAAAA TTTTATATGT TGGCTTGTTA TGTTAAGGGA ATTAACATGG      240
TTGTCTTGTT TATATTATGT GATTCAAACA TTACTAGTCT TGGTAAATCT AATTCGTAAA      300
ATGCTAAATC TAACCATCTA TTAAATTTAA AACC      334
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(2) INFORMATION FOR SEQ ID NO: 4262:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4262:

TTTCGGTCAT ATTCAAACGT TTTCACCTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT	60
ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGG TCTCAATGCG GTCATCGCA	120
TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGnAGTA ATTGGGCTAC CATCGTCGCT	180
AAAGACCTTT CTTGACTTGT GACAATCGCT TGCnTCTTTC CTCTCCTTCG GCTCTCGCTT	240
ACTCATtnAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT	300
TTCACCTTCGC CAAGCCATTT TTCTTTGTGT	330

(2) INFORMATION FOR SEQ ID NO: 4263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4263:

GAGGTATACC CCGGGACGGC TGAAGGGGAT GAACCCTAC GnAATGTCGG AACCACAATC	60
CGATGTGTTA CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC GAACCCACAC	120
CAAAGGTTTT GGAGACCTCT ATTCTACCGT TGAACTATGC CCCTATTAAA AATAATAAAT	180
GGAGGGGGGC AGATTCGAAC TGCCGAACCC GAAGAGTCGG ATTTACAGTC CGCCGCTTT	240
AGCCACTTCG CTACCCCTCC ATAAATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC	300
TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG	339

(2) INFORMATION FOR SEQ ID NO: 4264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4264:

GTATTTCAAA GTAAAATTAC ATGTTAATAC GTGnTTAATG GGCGAGACTC CTGAGGGAGC	60
AGTGCCAGTC GAAGCCGAGG CTGAGACGGC ACCCTAGGAA AGCGAGCATT CAATACGAGA	120
TnTnATGAAA TAGAGAACAG CAGTAAGATA TTTTCTAATT GAAAATTATC TTAGTGCTGT	180
TTTTTAGGGA TTTATGTCCC AGCCTCTTAC TCTAATTATA TTTACTATCA ATTAGACAAA	240
ATGGCCATTT TCAAATATCA CGCGTTGTTT CTACCTTGA ATATATTTAT TATAATTCTC	300
TTTTTGAAA ATCAGTTAAC ATTAATTTAG ATGTACCGTA TTTTAAACAC T	351

(2) INFORMATION FOR SEQ ID NO: 4265:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4265:

```
ATTTTCACTT TAAACCTGC TTCTTTGGCT TTTTGCATAT AATGTTGCGA TTGTTCTATT      60
GTAAATACAC CTGTTTCACA GAAAATATCC GCAAAGTCTG CATATTGTTT TATCTCCGGA      120
AGTAACGCAA TCATTTCTTC TAAAAATGCC TCATTTGAAC TTGCCTCTTT AGGTACAGCA      180
TGAGGCCCTA GGAAAGTATG TTTTCATGTCT AAATCATATT TCTCAGCTAA ACGnTTAGAC      240
ACTTTCAATT GCTTCAGTTC ATTTTCTCTA TCTAATCCAT AAACCACTCT TGACTTTCAA      300
CTGCAGTCAC GCCGTGTTTn AATCCATAGT AAGACAAAnC ATGACT                        346
```

(2) INFORMATION FOR SEQ ID NO: 4266:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4266:

```
TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT TTATTGAAAA TGGTGCCGAG      60
GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGGAT TTAAAGTCCT GTGCGTCTGC      120
CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CGGGATTCTGA ACCCGCGACC      180
CCAACCTTGG CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA      240
GTCGAACCCC CACGCCGTAA GGnTGAGATC CTAAGTCTAG TGCGTCTGCC AATTCCGCCA      300
CACCCGCCAA TGGTGAGnCA TAGAGGnTTC GAACCTCTGA CCCTCTG                        347
```

(2) INFORMATION FOR SEQ ID NO: 4267:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4267:

GACTTGTTCT CTTGGACCTA TATCATGTTC TTTATTTTCT AATGCAGGAT CTTTAATTGC	60
ATCTTTAAGT GATTCATCCG CTGCAGGATA GTTTTTCGCA GTGTTTGCTG GTTGCGTGAG	120
GTnTGTGTTT GATTTGTATC CTTAGGTGGC TGAGTTGTAG TTGCATTATT ATTTTGATTT	180
TCCGAGATTT TATCTGAAGT ATTTGTATTT TCTGCTGCTT GTGCTTGATG TTGAGAAGTA	240
ATTAAAAATA GTGTACTGAC AATGACCGAT GCAACGCCTA GAGTTGATTT TCTAATAGAA	300
TAGGAAAGAC CnTnAATTTT GGGTGGATGT TTGTTCA	337

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4268:

ATACATGTTG GAATACTTGT CCCATAGAnA ATATTGGCTG GTAACCCAAT CACGGCTTCT	60
AAGTAGTTCT TTTCTTCTAT TAAATAGCGA CGAATCACAC CTTCTGCGGC ACCACGGAAT	120
AATACACCAT GTGGGAGTAC GACTGCCATG GTACCTTCAT CGTCTAGGTA ATGTACCATG	180
TGTTGAATAA AGGGCAAAGT CTGCTTTGGG ATTTTGGCGC AACTTGGCCG TAACCACTG	240
GAATCGTTCA TCATTTTTCA nATTTTGGAA TCTGGCTGGT TCCATTTTCG GCACTGGTAT	300
GGTGGGGGTT TCGGCAATAA ACGGCATTCA AATGGTATTT GGCCTAAACA AGGCCGGGAT	360
TTTTCCAATG GGGGTCATCA TTAAAnGGGAT CnTCGAAGTT	400

(2) INFORMATION FOR SEQ ID NO: 4269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4269:

GGCTCATCGC ATCCTGGGGC TGTAGTCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG	60
CGGTACGGAG CTGGGTTTCA AACGTCGTGA GACAGTTCGG TCCCTATCCG TCGTGGGCGT	120
AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG	180
TACCAGTTGT CGTGCCAACG GCATAGCTEG GTAGCTATGT GTGGACGnGA TAAGTGCTGA	240
nAGCATCTAA GCATGAnGCC CCCTCAAGAT GAGATTCCCA ACTTCGGTTA TAAGATCCCT	300
CAAAGATGAT GAGGATATAG GTCGAGGTTG GAGCATGGTA CATGT	345

(2) INFORMATION FOR SEQ ID NO: 4270:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4270:

AAGAATTAAT TATACATTTT ATTAACATTT AAGTCAATAA CTTTTTTTCT CTTGTCCATT	60
TTATTTTTTTA ACCAAAATTT GATTAAAAAA CTGCCTGGCA ACGTTCTACT CTAGCGGAAn	120
TAAGTCGaCT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG	180
TGACCTCctT GCTATAGTCA CCAGACATAT GaATGTAATT TATACATTCA AAAC TAGATA	240
GTAAGTAAAA GTGGATTTTG CTTCGCAAAc ATTTATTTTG ATTAAGTCTT CGATCGATTA	300
GTATTCGTCA GCTCCaCATG GTCACCAGCT TCCACCTCGA ACCTATTGGn CGCATCATCT	360
CGCAGGGAnC	370

(2) INFORMATION FOR SEQ ID NO: 4271:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4271:

TGAGGTACGT CCAGAATnGG GATGGCTAA AAATGCATCA TTTATAATTG GACGACGCCA	60
ATTAACAAAA GGCATTGATT TAGAAGGGCG GACATTTTTTA CACAATTATG ATTGGCGTAA	120
AGATAAAGAT GGCACATTAT TAAATACCAT CATTTCTGGT CCGGCACTTG TGGCACAATG	180
GaTTAATTTA CAATATTATG CGTCGACAGT TGCGCCGCAT TTTTaCGGtAATGGGAATAA	240
AGCGACACAA ACCGTCACGT CAGTGTGGT GTCATGCAAG GTAATGCGAG TGCATCTGAT	300
GTAGGGCTTA TCATGGCCAA TCTGTTA	327

(2) INFORMATION FOR SEQ ID NO: 4272:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4272:

CATTCTTTAA ACTCTGTAAG TACTTCTTCA ATCTCAGGGG CATCTACTAA CATATCATCA	60
GTAATATGCG TCAAATTGAT AATCGTTTCC GATAATCGTT CATGCGGATT ACTAAACCTT	120
TCAAACCTTAT CGATGATTTT ACCGTTATGA ACTTTCACAG CTGCAAnTCG ATGATTTTAT	180
CATACTGATT TGATAAACCA GTTGTCTCAA CGTCGAACAC AACATAAGTA GCATCTTTTA	240
ATACGACATC TTGTGGGTTG TATGCAATCG GGAACACCAT CATCAACTAA CATACCTTCC	300
ATACCGGnAT ATCATTTTAA nGCCA	325

(2) INFORMATION FOR SEQ ID NO: 4273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4273:

TCCGGCCTTG ACCTGAAGAA CACTTGTCTT GTCGTTAAGA TGACTCTAGA CTCTTATGTT	60
TATTATCAAC CGTTAATAAA CTTACCATCA AGAGTGCACC TACCC CA ACT GACAGTGCAG	120
TATAGAATGG TGTCATACCT GAACCATAAT CCTTAACTGG GAAAACATCA ACAGTCTTCT	180
TATTAATAGG ATTTGCAATA ATACCCGCTT GCTTTTTTCAA ATCATTCTTA AGTGTGTCGA	240
TnAATTTGTC GACTGCATCA TCTnTGTCTA ATTTCTTGAA AATTTTGATT CGCTTTTTTC	300
CAAATCCTTn TCCAACATCA GGCAATTTTA TTTTGAGAAA AATCAGCCAA ATCCGGA	357

(2) INFORMATION FOR SEQ ID NO: 4274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4274:

ACGTTAGCAC AAGCCATGAA CCAATTAGGT GGAAAGAGTA ATAGTGGTGA AGGTGGCGAA	60
GATGCAAAAC GTTATGAAGT ACAAGTTGAT GGAAGCAACA AAGTAAGTGC GATTAAACAA	120
GTTGCTTCTG GGC GTTTTGG TGA ACT AGT GATTATTTAC AACATGCCAA AGAAATTCAA	180
ATTAAAGTTG CGCAAGGTGC AAAGCCTGGT GAAGGTGGTC AATTACCTGG TACTAAGGTA	240
TATCCGTGGA TTGCGAnGAC AAGAGGGTCA ACGCCAGGTA TCGGTCTGAT TTCACCACCG	300
CCACATCATG ATATTTnATT CCATAnGAGG ATTTAGCCGC CACCTGA AC CTGGATTTTG	360

GAAAAATGGC GAATTAAGGT TGCnGATTTT CCCCGGGTAA 400

(2) INFORMATION FOR SEQ ID NO: 4275:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4275:

AACGTCGTTA ATTGAATAAC GCTTATGTTA TAAGAGCACT CATACCAAAC CATAATCATC	60
TATAGATATA ACAATTCACG ATATAAGGGC TGTGTTTGGC ATAGCCTTTA GATATACACT	120
TAATTCCTAT TAAAATAGTA GGGATTAAAA GGGGGCTTGT CATGGATTAA AATTCAACAA	180
TTACAACATC ACTTTGGATC ACATAAAGTA ATTCATAACT TTAATTTGGA CATTAGCAAG	240
GGAGAAATAG TCACTTTCAT AGGGGAAAAG TG GTTGC GGA AAGTCTACTT TACTCAATAT	300
TATCGGTGGA TTTnTTCCAT CCATCnCTG GTCGTGTCCA n	341

(2) INFORMATION FOR SEQ ID NO: 4276:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4276:

TAGTGATATA CGACATCACA GCATAATATT GCTTTAGAAA GTCGTGCCGA ACTGGAACCTT	60
ACAAGTCTAG TTCGAACACA CACTGATGTG AGTGGTTTTT TTTATTTTAA ACATGAACAA	120
TCAGATAAGT TACTAGCATT AGCAAATATT ATTAAATCAA AGGGTTCGA TTCATAAAAT	180
TTAAAACAAT GATTAAAATT AGACGTGTAA ATTGTTAAAT TCTAAAACGG AAATAACCAC	240
CATTCCATTA AACCACTTTT TTGTTTCATCA CTATATTTCA CACnGCTTCA TTAATAAACG	300
GAATGCTTCA nCCGCTTCAA CTTCAACTGG CTTCAACTTC nGCCTACTTC ATCATACCAA	360
ACGGTCCG	368

(2) INFORMATION FOR SEQ ID NO: 4277:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4277:

ATGGAAGTAC GTGACGTTCA CTA	CTCTCAC TATGGCCGTA TGTGTCCAAT TGAAACACCT	60
GAGGGACCAA ACATTGGATT GATTA	ACTCA TTATCAAGTT ATGCACGTGT AAATGAATTC	120
GGCTTTATTG AAACACCATA TCGTAA	AGTT GATTTAGATA CACATGCTAT CACTGATCAA	180
ATTGACTATT TAACAGCTGA CGAAGA	AGAT AGCTATGTTG TAGCACAAGC AA	240
ACTCTAAA TTAGATGAnA ATGGTCG	TTT CATGGGATGA TGAAGTTGTA TGTCGTTTCC GTGGTAACAA	300
TACAGTnATG GCTAAAGn		318

(2) INFORMATION FOR SEQ ID NO: 4278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4278:

CACTTGTACT TTCTGATGTT GAGCC	AGACT CTGATGTACT TACCGATGTA GATAAACTTG	60
CAATGGTCGA CATGCGGTTT GAAGT	TGATG TACTTAGCGA ATCACTTAAT GATGCTGATG	120
TGCTTTGTGA ATCGGATTCTG CTCG	TGCTTG TACTTGTTGA GTTTGAGGCA CTTTGGCTTG	180
CTGAGTTTGA GTCTACTCCG CTTTG	ATTCA TTGAGGCACT TAGTGACAAT GATGTACTCG	240
TTGAGTCAGA CAAACTTGTA CTCGT	TGACG TACTTGTA CTCTGATGTT GATTGAGACA	300
TACTTATGCT CATTGGATGT TGAAT	CGGAT TTACTTTCAC TTGAATGATG TTGAGTCGGA	360
TTCACTTTCA CTTGTAGAAC CACTT	AATGA TGTGGGATGT	400

(2) INFORMATION FOR SEQ ID NO: 4279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4279:

TTTGTACTTC GATTTAAAAG ATATT	AGACA TAAAATCTAA AAnCAGCAGT AAGATGATTT	60
ATGATTAAAA ACTATCTTAC TGCTG	TTTCTAC TTTTATAAT ACTTCTGAAT GTCTTCACTT	120
ATACTTCTAG TCACAGATTT AAATA	ATCAA AAGTGCACAT TATAAAATA TCAATTTTAC	180
ACTCAATGCG GCTCATCGCA TTCAT	TTTCTT GTCTAGCAAC GTTCTACTCT AGCGGAAGTA	240

AGTTAGCTAC CATCCTCGCT AAGAACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC 300
CTCTCCTTCG GCTCTCGCTT ACTC 324

(2) INFORMATION FOR SEQ ID NO: 4280:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4280:

CTCACTAGTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60
GTGGATTGTC CTTTGGCATG TGnTTAGGAG AGCGTTCTAA GGGCGTTGAA GCATGATCGT 120
AAGGACATGT GGAGCGCTTA GAAGTGAGAA TGCCGGTGTG AGTAGCGAAA GACGGGTGAG 180
AATCCCGTCC ACCGATTGAC TAAGGTTTCC TGnGGAAGGC TCGTCCGCTC TGGGTTAGTC 240
GnGTCCTAAG CTGAGGCCGA CAGTAGGGCG ATGGGATAAC AGGTTGATAT TCCTGTACCA 300
CCTATAATCG TTTAATCGAT GGGGGG 326

(2) INFORMATION FOR SEQ ID NO: 4281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4281:

TCGAACATGA GCGATTATTT CTTATGAATT CAAGCTTAT TAAAACTCTT TATTTCACTCG 60
GTTTTGCTTG GTAAAATCTA TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG 120
GTGGGCCTAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGCGTGCG CTCTAACCAG 180
CTGAGCTATA GGCCCATTTT TTTGAATGTT AAATAAACAT TCAAACTGG AATACAATAT 240
GTCACGTTAT TCCGCATCTT CTGAAGAAGA TGTTCCGAAT ATATCCTTAG AAAGGnAGGT 300
GATCCAGCCG CACCTTCCGA TACGGGCTGA CCTTGTTGAC GACTTGCACC CCAAGCATTT 360
GTGCCCA_nC_n 370

(2) INFORMATION FOR SEQ ID NO: 4282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4282:

```
GAGAGATGAC ACGGnACTGA ATTGGTTTGA CACCACGTGA TGAATGTGAT CGTCGGCCTT      60
CTTCACGATT GnAATACTTT TACATCAAGA ACGATACCGC CAGCGCCGTG AGGTACACGT      120
AATGAAGTAT CTCTAACTTC ACGTGCTTTT TCACCAAAGA TTGCATGTAA CAATCTTTCT      180
TCGGCAGTTA ACTCAGTTAC ACCTTTAGGC GTTACTTTACCACTAAAAT ATCTCCATCT      240
TTTACTTCTG CACCAATATA AACGATACCA CGATCGTCTA AGTTCTTAAG TGCACCTTCA      300
GAAACATTAG GnATATCTCT TGTGATTTCC TCAGGGCCTA ACTTAGTATC ACGTGCCTCT      360
GAATCCATAC TCCTTCAATA TGAATAGAAG TATACACGGn                               400
```

(2) INFORMATION FOR SEQ ID NO: 4283:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 324 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4283:

```
AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA AAGAGAAATT GGATTCCCAA      60
TTTCTACAGA CAATGTAAGT TGGGGTGGGA CGACGAAATA AATTTTGAGA AAATATCATT      120
TCTGTCCAC TCCCGATTAT CTCGTCGCAA TATTTTTTTC AAAGCGATTT AAATCATTAT      180
CATGTCCAAT CATGATTAA ATATCACCTA TTTCTAAATT AATATTTGGA TTTGGTGAAA      240
TGATGGACTC TTTGCCTCGT TTAATTGCCA TAATGTAAAT nCCATATTGT GCTCTTATAT      300
CTnAATCCAT GATAGACTGn CCCG                                              324
```

(2) INFORMATION FOR SEQ ID NO: 4284:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4284:

```
AAATCGTAAC GAGTGAAC TTCTATTTAG GTGGCGAGT AACTTACTAG CACCTGACGA      60
AACGGTTTTA GATCGTATTC AATTGAAAAG GCCGGTATTG AATGAATCAC ACTTAGCAGC      120
GATTGATCAG GAACATTTTA AATTAACCTA TTTATCAACG GTATATGAAG GGGATTTGGC      180
```

AAGATGCGTT ATAAGCATTA GGCCGTAGAA GCAGTGAAAT GCTGTnAAAC AAGGGCGCTC	240
AAATTCTAGT GTTAGATGAT AGTGGATTAG TTGGATAGCA ATGGCTTTGC AATGCCGATG	300
TTTACTCGCA ATGAAGTGCA TGTGCCATGC AATTGACTTC TTAAAGCCA GATTTACGTG	360
ATGTCTAACA AGTTTTnTnC GCTAAAATCn GGGTGGAGAC	400

(2) INFORMATION FOR SEQ ID NO: 4285:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 560 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4285:

CATTTTTCTT TGIGTTTACT TTTTATTTTG ACGTTTTAGA CATAAAAAAA GAGACTCACG	60
GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC	120
TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCATCTTT CCTCAnCATC GGnTnTAGCT	180
TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCT GTTTCGTCAG ATTCAAACGT	240
TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA	300
AAAAAAGAG ACCTTGnCGG TCTCAATGCG GGCTCATCGC ATCCATTTTT TGCCTGGCAA	360
CGTTCTACTC TAGCGGAAGT AATTGnGCTA CCATCGTCGC TAAAGACCTT TCTTGACTTG	420
TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA	480
ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT	540
TTTCTTTGTG TTTACTTTTT	560

(2) INFORMATION FOR SEQ ID NO: 4286:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4286:

GTAACACTCG GnATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GTAGCTAATA	60
CCGGATAATA TTTTGAACCG CATGGTTAAA AGTGGAAGA CGGTCTTGCT GTCAC TTATA	120
GATGGATCCG CGCTGCATTA GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA	180
TAGCCGACCT GAGAnGGTGA TCGGCCACAC TGGAAGTGAACACGGTCCA GACTCCTACG	240

GGAGGCAGCA GTAGGGAATC TTCCGCAATG GGCGAAACTG GACGGAGCAA CGCCGCGTGA	300
TGnATGGAAG GTCTTCGGAT CGTAAAACTC TGTATT	337

(2) INFORMATION FOR SEQ ID NO: 4287:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4287:

CAATCGTGCT CAnTGCGCAT CGTnACTCAT CTGTATGTGT TCCAGCATAT ACAATTTTGC	60
CATCTTTAAT GACAACTGTA CCATTTTTC CAACATTTAA TTCATCTAAT TCCTTACCCT	120
TCAAAGGTTT ATCTGTTGAT CTCGGTAAAA TTAATTCTGG CTATATGATT AATTATTAAA	180
TCATCATTAC TTATCACCTG CTTTATCAAT CATGGAATAT GAATACCTTT TTCTTTAGCT	240
GTTTGAATAG CGATGTCATA GCCAGCATCA ACATGTCGGG CAACACCCAT ACCTGGGTCA	300
GTCGTCAATA CACGTTCCAA TCTTCTTTC GCACGCTCTG AATCCATCTG G	351

(2) INFORMATION FOR SEQ ID NO: 4288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4288:

CTATTCACTG CGGCTCTTCT GGGCGTTAAC CCTAAAGAGC ACCCCTTCTC CCGAAGTTAC	60
GGGGTCATTT TGCCGAGTTC CTTAACGAGA GTTCGCTGC TCACCTTAGA ATTCTCATCT	120
TGACTACCTG TGTCGGTTTG CGGTACGGGC ACCTATTTTC TATCTAGAGG CTTTCTCGG	180
CAGTGTGAAA TCAACGACTC GAAGACACAA TGTCTTCTCC CCATCACAGC TCAGCCTTAA	240
CGAGTACCGG ATTTGCCTAA TACTCAGCCT TACTGCTTAG GACGTGCAAT CCAATCGCAC	300
GGTTTnGCCT ATCCTA	316

(2) INFORMATION FOR SEQ ID NO: 4289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4289:

TTnTTTATGT CTAAAACGTC AAAATAAAAG CAAACACAAA GAAAGATGGC TTGGCGAAGT	60
GAAAACGnTT GAATCTGACG AAACGAGAAA TGTAAGTAT AATAAAAAGC AGTCATAAGA	120
TGATTTCAAT TAGAAATCAA TTTATGACTG TTTTCTTAC TATGTGTTAA ATTAACAATG	180
AATATAACAT CTTATTTTCA TTAATATAAA TATTGGAAGG ATCGAnATGA TTTACACGTT	240
GTTTGAGTTG TATTAAATCA TCATGATCTT TAAGTTGAAT ACCAATAATG ACAGTACCTG	300
TATTTTGAGA GATTTTTTAA GT	322

(2) INFORMATION FOR SEQ ID NO: 4290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4290:

TCATTTAGCT CTACTAAACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT	60
CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT AGGCATAAAA	120
AAAAAGACCT TCGGGTCCAA TGCGGCTCAT CGCATCCATT TTTGCCTGG CAACGTTCA	180
CTCTAGCGGA AnTAATTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC	240
GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCnACT AAACTCGTTG	300
CGCTCTTnTC TCGTTTCGTC AGATTTCAAA CGTTTTCA	338

(2) INFORMATION FOR SEQ ID NO: 4291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4291:

AATTGGTTTA CACCAGGTGA TAATGTATCG TCGCCTTCTT CACGATTGAA TACTTTTACA	60
TCAAGAACGA TACCGCCAGC GCCGTGAGGT ACACGTAATG AAGTATCTCT AACTTCACGT	120
GCTTTTTTAC CAAAGATTGC ATGTAACAAT CTTTCTTCGG CAGTTAACTC AGTTACACCT	180
TTAAGGCGTT ACTTTACCAA CTAAATATC TCCAETTTT ACTTCTGCAC CAATATAAAC	240
GATACCACGA TCGTCTAAAG TTCTTGAAGT GCACTTTnCA GAAACATTGA GGGAATGATC	300

TCTTGTGATT TCTTCCAGGT CCTAACTTGA GTGATCACGT GGCTTCTGGA TTGCAGACGC 360
 TTGCAAGATG GAATGAGAAG TGAnACACGT GCATCCTTGC 400

(2) INFORMATION FOR SEQ ID NO: 4292:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4292:

AAACGTTTTCT ACTTCGCCAA GCCATTTTTCT TTTGTGTTTA CTTTTTATTT TGACGTTTTTA 60
 GGCATAAAAAA AAAGAGACCT TGCGGTCTCA AATGCGGCTC ATCGCATCCA TTTTTTGCCT 120
 GGCAACGTTCT TACTCTAGCG GAACGTAATT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 180
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC 240
 TACTAAACTC GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTCT ACTTCGCCAA 300
 GCCATTTTTCT TTTGTGTnnA CTTTnT 326

(2) INFORMATION FOR SEQ ID NO: 4293:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4293:

GGGGACAATT CCCTGGGGGT TCAAGTCCTC TGGGCGGCGC ATCAAAATTC TTAATTTAAA 60
 TAAGCGGGTG TAGTTTAATG GCAAAACCTC AGCCTTCCAA GCTGATGTTG TGGGTTTCGAT 120
 TCCCATCACC CGCTCCATAG ATAATTTTAA TGAACATTGA AACTGAATG ACAATATGTC 180
 AACGTTAATT CCAAAAACGT AACTATAAGT TACAAACATT ATTTAGTATT TATGAGCAA 240
 TCAAAACATCA TAATTTTTAT GGAGAGTTTG ATCCTGGCTC AGGATGAACG CTGGCGGCGT 300
 GCCTAATACA TGCCAGTCGA GCGAACGGAC GAGAAGCCTG CCTCnGnGAT GTTAGC 356

(2) INFORMATION FOR SEQ ID NO: 4294:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4294:

TTATCACCCA TGTCTGACT CCCAAGTTAA ATTAATTGGC ATTCGGAGTT TGTCTGAATT	60
CGGTAACCCG AGAGGnCCCC TCGTCCAAAC AGTGCTCTAC CTCCAATAAT CATCACTTGA	120
GGCAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATTTCC AGGTTTCGATT GGAATTTCTC	180
CGCTACCCTC AGTTCATCCG CTCACCTTTT AACGTAATCG GTTCGGTCCT CCATTCAGTG	240
TTACCTGAAC TTCAACCTGA CCAAGGTAGA TCACTGGTT TCGGGTCTAC GACAAATACT	300
AAACGCCCTA TTCA	314

(2) INFORMATION FOR SEQ ID NO: 4295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4295:

AAGTGAAAGA ACTCGGCGTG ACACCTATTG CACGATTCGT TGGTTTTAAG GCAGTAGGCG	60
TTGACCCGAA AATTATGGGT ATTGGGCCTG CATATGCGAT TCCTGAAGTA TTCACTCA	120
GCAATCTATC TGTGAAGAC ATTGATTTGA TCGAATTGAA CGAAGCATTT GCTTCTCAA	180
CGATTGCATC TATTAAAGAA GTAGGTCTAG ATATATCACG TACGAATGTG AATGGTGGCG	240
CTATTGCTTT AGGTCATCCA TTAGGTGCTA CAGGCGCCAA TGTTAACCCG CGCGTTTACC	300
TAATGAAATG GGGTAAACCG nCCCGATAGn CCGTAnCGCA AGGGT	345

(2) INFORMATION FOR SEQ ID NO: 4296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4296:

TAAATTGATT TCTAATTGAA ATCATCTTAT GACTGCTTTT TATTATACTT TACATTTCTC	60
GTTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATC TTTCTTTGTG TTTGCTTTTA	120
TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC	180
ACTTTTTGCC TGGCAACGTT CTACTCTAGC GGAAnTAATT CGnACTACCA TCGACGCTAA	240
GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGGCT ATAGTCACCA	300

GACATATGAA TGThAATTGA TACATTGCAA AACTAGGATA GTGAAGTAAA AGTGATTTG 360
C 361

(2) INFORMATION FOR SEQ ID NO: 4297:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4297:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAAC TTTTCACTT CGCCAAGCCA 60
 TTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG 120
 TCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 180
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 240
 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300
 TTCACTTCGC CAAGCCATTT TnCTTTGTGT TACTnT 337

(2) INFORMATION FOR SEQ ID NO: 4298:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4298:

GTATTCCTCC ATTATTATAG GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA 60
 CGGGAATCCT GCGTGACAGn CAGGCGTGTT ACCGCTACAC TACGAGACCA TTAGTAAAC 120
 GGAGGAAGAG GGATTCGAAC CCCC GCGAGC CGTTAAGCCC CTGTCGGTTT TAAGACCGA 180
 TCCCTTCAGC CGGACTTGGG TATTCCTnCA AAATTATATG GACCTnGCAG GACTCGAACC 240
 TGCGACCGAA CGTTATGAGC CTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT 300
 TTTTACAAC TATAAAATAG TGG 323

(2) INFORMATION FOR SEQ ID NO: 4299:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4299:

CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT CCATTAAATG	60
AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT AAAATTGCCT	120
ATAAATTTTT AGCACATAAA ATAAGAGGnG CCAACCATTG TTAGACTATA ACAACGGTTG	180
GCTCTTTAAT TGTA AAAAAGA AAACCATAcG CTATGnTGTT ACAAnGAAAA AGGTTCTACC	240
ATTGTCACAA AAAATGCATC TCTACGTGCT AGAATAAATA TTGGTCAGCC AACCAAAATA	300
ATCAACACGA GGAGATGCTA TTT	323

(2) INFORMATION FOR SEQ ID NO: 4300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4300:

CTAACATACC ACCTACAAGA CCTGAAGCGA AACCAGGTTT ATCCGCA AA CTACGTGCAA	60
TGAATCCAGA TAAAATTGGA ATGATTAACG CGAATCACTT TTA CT ACCAA TGTTCCAAAG	120
CTGCTCTGCA AACGCATTGT ACTCTGAGCT TTTTGGATTA AATGAATTTG CTCCAAATAA	180
AAATACAATT GCCATTAAAA TACCACCAGA TATTACAAGT GGCAACATGT TAGAAACACC	240
GTTnCATTTGA AGTGTTTGAT AGAATGCTTT ACCTGGGGCT TGAATTTTTTC TTGGACTGTG	300
CATTTGAGTT ACCTTTTCTT TGGACCATCA CGGGGCAACA AAAGGTTTGA CGACTTGTGA	360
GCTGAATGGC TTnGnTGAAT GAATT	385

(2) INFORMATION FOR SEQ ID NO: 4301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4301:

TCCTGTACCA CCTATAATCG TTTTAATCGA TGGGGGGACG CATAGGAATA GGCGACGTGA	60
CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA	120
GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTT CACTGCCGA	180
GAAAAGCCTC TAGATAGAAA ATAGGTGCCC GTACCGCAA CCGACACAGGTAGTCAAGAT	240

GAGAATTCTA AAGTGAACGA ACGAACTCTC GTTAAGGGAC TCGGCAAAAT GAnCCCGTAA 300
 CTTCTGGGGAA AAGGGTnCTC TTTAnGGTTA ACGCCCCAAA AAACCGCT 348

(2) INFORMATION FOR SEQ ID NO: 4302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4302:

AATGGAACGT GCTTCTGTAT TGGCCCAAGT AGATATTCAT CGTGCAGCAA CACATAATAA 60
 AGGTGTTATG AATGGCATAAC ATGCTGTTGT TTTAGCAACA GGGAAATGAT ACGCGTGGTG 120
 CAGAAGCAAG TGC GCATGCA TnACGCGAGT CGTGACGGGA CAGTATCGTG GTATTGCTAC 180
 ATGGCGTTAC GATCAAGATC GTTCAACGAT TGATTGGTAC AATTGCAAGT GCCTATGGAC 240
 ATTGGGCAAT CGTTGGCGGT GGTACAAAG TATTACCAAT TGCTAAAGCT TCCATTAGGn 300
 GCTGACTAAA TG TAGAGTCA GCACAAGAAT TGAGGTCCAT GTTAGTTGGC TGCCGTTGGG 360
 TTTTGAGCGG CAAAAACTTT GnCAG 385

(2) INFORMATION FOR SEQ ID NO: 4303:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4303:

AGTGCGACGA TTGGTATTTT ACAAGAATTT TATCAACAAG ATTTAÆTAG CTAAACGCA 60
 GCAATCCCTG TGTTACTAGG CGATAACATT GGTACCACGA TTACAGCTAT CTTAGCTAGT 120
 TTAGCCGGCT CAATCGCTGC AAAACGTGCG GCGCTTGATC ACGTCATCTT TAACTTAATC 180
 GGGGTAATTA TCTTCACAAT TTTCTTGCCA GTTGTGATTC ATTTGATTAG TTTGTTACAA 240
 GATTTATGGG CACTTAAAC CAGCGATGAC GATTGCAGTA TCACATGGnA TCCTTCAACA 300
 TAACCAATAC CTTGGATTCC ATTTACCAAT TTGTAGCCnG GTTTAGCATn GGATTGGTTA 360
 CCAAGCCTTG TCCC 374

(2) INFORMATION FOR SEQ ID NO: 4304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4304:

AAAACAGGAT ACTTCGATAA GTAATGATT TCTGTTGTGA ATCGCGCACC ACGTTTCTTA	60
ATTTTACCGA CTATTATATT AATTGGTATT TTAGGTAGTA CAGCCGGCGA TGCTGCGACA	120
ATTTCTTGCC GCCGCTTGCA GCAATGCTTT TTATTAAAAT TGGCTATCAC CCTATCGCTG	180
GACTAACGAT GGCATATGCT TCCGCTGTTG GAGGATTTGC AGCAAAT TA GTTGTGTTGTA	240
TGCAAGATGC TTTGGTCTAT TCATTTACAG AACCGGCAAC ACGTATCGTT TCAGATTCTA	300
TTAAAACAAA CGTT	314

(2) INFORMATION FOR SEQ ID NO: 4305:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4305:

CGTTGCAGAA TGTGTTGAAA TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG	60
CCATTAATTT ACGGTTACCA ACCAATATAT GGTGATGATC AATCGTTGCT TCAATACCAT	120
GGCCAGGTAC TGCTTTAAAT GTTGTTGTCT CAGTTAATAT TAATTGCTTT TCTTTTGCAT	180
AATTGACAAT GGCTTCTGCC AATGGGTGTT CAGAATCTTT TTCAGCAGTA GCAAGTAGTT	240
GTAGCGTTTG ATTGTCACCA TGATAATCTG TCACGACTGG GACGACCATT TGTAATGGnA	300
nCCGTCCTTA TCTAAAACGA TGGGTATCAA TTTGATGnGG GCGG	344

(2) INFORMATION FOR SEQ ID NO: 4306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4306:

AGTTTCCCTG AAAATTAATC AAGGACTTAA CATTGCGAGT CAAGGTATTG ATCAAGCTAA	60
TGGACAGTTA AATGATGCCA AAGCTTCGTC ACACAAGTTA GAA T AGAGT CGGTGATTAT	120
CAAGATGCAA TTCGACGCGC GCAAGATTTA AATCGAAGAA ACCAGCAACA GATTCCTCAA	180

AATAGCGCGG CGAACAACGA AACATCAAAT AGTGCACCTG CAGCTGGTAA TGGTGTAGCA	240
TCAACGCCAC CAAGTGCACC AAGTGGCGAT ACTGCACCAA ATAATAATGT TACGCAAAT	300
ACCGCACCAG ATGAGTGAAT AATGCGCCTG TATCGACTAC ACCACAAATG ACAnCCGGG	360
GAAAnAGATGG TCAAATTT	378

(2) INFORMATION FOR SEQ ID NO: 4307:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 basepairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4307:

GGACTTGGGT ATTCTCCAA AATTATATGG ACCTTGCAGG ACTCGAACCT GCGACCGAAC	60
GGTTATGAGC CGTTAGCTCT AACCAACTGA GCTAAAGGTC CTAnATATAA TTTTACAACT	120
AATAAATAGT GGCGGTGGAG GGGATCGAAC CCCCACCTC ACGGGTATGA ACCGTACGCT	180
CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG	240
GATCGAACCG CTGGACCTCC TGCGTGGCAA AGCAGnCGCT CTCCCCTG nGCTAAGCCC	300
CCATAATAAT TACAGTAT	318

(2) INFORMATION FOR SEQ ID NO: 4308:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4308:

TGTACGTTTA ATACCTATGA TATATGCTGC AAGTCTCATA TCTATTTTTC GGTTTTGAGA	60
CAATTCGTAA ATCGTATCAA ATGCCGCTTC TAATTTTTC CGTAGCTTTT CATTAACCTC	120
TTCTTCAGAC CAATAATAAC CTTGATTATT TTGTACCCAT TCGAAGTAAG AAACCGTTAC	180
ACCACCAGCA CTTGCTAATA CGTCTGGAAC TAATAATATA CCACGTTTAC TTAAAATACG	240
TGTTGCTTCT GGTGTTGTAG GTCCATTAGC AGCTTCAACA ACGATACTAG CTTTAATATC	300
ATGTGCATTG TCCTCnGTAA TEGGTTGAA TAGCGnGGGA CTAAATGCAC ATCnAATCAA	360
CAATCCTATT GGATGTCCCA AnAATTGTAC GACCAACACC	400

(2) INFORMATION FOR SEQ ID NO: 4309:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4309:

CAAATAAACC AGAGCTAGTT GCAATTGCTG AACCACATCC TAATAGACCG AAAAAGAGAA	60
GTAGACGTGC GGCACCGGCA GATCCTAATG CAACTCCAGC AATCCAGCG GCTGCAGCGG	120
GTAGGAAACG GTGGTGCACC AGTTGCAATT ACAGCGCCAT ATACGCCAAC AACTGATCCT	180
AATGCCAATA ATGCAGGACA AAATGCACCT AACGAATnGT TGTTCAATTTG ATGACAATGG	240
TATTAGACCA AGTACCAACC GTTCTGTGCC ACnTnAAACG TTGTTAATAA CTTGCCGGGC	300
TTCACACTAA TCAATGGTGG CAAAGT	326

(2) INFORMATION FOR SEQ ID NO: 4310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4310:

TCAAAGCGCC AATAACATCT TCTACTGAAG TTTCTTTAGA TTTAGCATTG AGTGATAATG	60
TTATTGTTGC TTTTCTTCC ATTGGAATAC TTTGATGAAT CGTTAATACA GATAGTTCTA	120
ACTTTGATAT AACATCTAGT ACACGTGCCA ACATACCAAC AATATCAGTT ACATATAAAA	180
TTAATGTAAA TTCTCGATGG TCAAGCATTT TATCGGCTAC TGGAAATATC GTTTCTCTAT	240
ATnTATAAnA AGCACTTCTA GATAGATCAA ACTGTTTAAC GGCATCATAA ATGGnCAATG	300
TCGGATCACT TTT	313

(2) INFORMATION FOR SEQ ID NO: 4311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4311:

GGTTCGAATC CAGCTAGCCC AGCCATTAGA GCCATTAGCT CAGTTGGTAG AGCATCTGAC	60
TTTTAATCAG AGGGTCAGAG GTTCGAATCC TCTATGGCTC ACTACTTGCA CTTTCCATTT	120

TTGGGAAGTG CTTTTTTTTTA GGTTCCTCCAC CAAATGTGGT GGGTATATAA TTAAAGAAC	180
TATTTTTTAAA ATACAACCTTT TAGAGCTTTT ATTATTAGGC GGCCAGTCCA TTATTGGGGC	240
TGGTTGTCTT CnTTTTTTTCT CCTTTGTACA AGCTGAAAAT CATCATTATA CGTGCTTAAA	300
GTGGTGAATT CTGAACCAAA GAATCACTTG ATAATTTATC TATATAATCC TCnATAGACC	360
ATATAATGCT GGAATAATGG ATCTACAnCC TGAGTTCCAn	400

(2) INFORMATION FOR SEQ ID NO: 4312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4312:

CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCGG AAATCTCTGG ATCAAAGCTT	60
ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA	120
AGGCATCCAC CGTGCGCCCT TAATAACTTA ATCTATGTTTCCACCATTTT TATAAGTCAA	180
ACGCTCACAT ACGGCTTCGT TTTCATTATT TTAAATGCTC ATTTACATAA GTAAACTCTG	240
CTTTAAAATA ATTAACATCAT TGTCTGChAA ACGTTTTCTnT TTATAAAAAG ATTAAACGCG	300
TTATTAAAnCT GTGGAGTG	318

(2) INFORMATION FOR SEQ ID NO: 4313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4313:

ACGGTGATCA CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GCCAGTTCCG CCACCCCGGC	60
ACTATAAAAA TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG	120
TATTCTACCG CTGAACTACT TCTGCATATG CGGGTGAAnG GAGTCGAACC CCCACGCCGT	180
AAGGCATAGA TCCTAAGCTT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC	240
CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCn	300
AATGGnTCTT CCATGG	316

(2) INFORMATION FOR SEQ ID NO: 4314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4314:

AGGAAAAGTC GTTGTGATAC ATCAACCAGC TGAAGAETA CCACCAGGTG GTGCTAAAC	60
AATGATTGAA AATGGTGTAT TAGACGGTGT TGATCATGTA TTAGGTGTAC ACGTCATGAG	120
CACAATGAAA ACAGGTAAAA GTGTATTACC AGACCTGGTT ATGTTCAAAC AGGACGCGCA	180
TnCTTCAAAT TGAAAGTCAA GGTAAAGTGG TCATGGTTCA TCACCACATA TGGCCAATGA	240
TGCCATTGTT GCAGGTAGCT ACTTCGTCAC AGCGTTACAA ACAGTGTATC TAGACGACTA	300
GGCCATTGTA ACCGGTGGTT TCACATCGGT CATTTnCCGT AAAAGnCCAT TCCATG	356

(2) INFORMATION FOR SEQ ID NO: 4315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4315:

TATCAGCATT TGTAAGTGT ATTGTTTATA ACTTCTGTGT GAAGCGCAAT ATTACAATTA	60
AAATGCCGAA AGAAGTACCG CCGAATATTT CACAAGTATT TAAGGACTTA ATTCCATTTT	120
CAGCGGTAAT CATCATTTCTT TATGCATTAG ATTTAGTCAT CGCAACAGCT TTAAATCAAA	180
TGTAGCGGAA GGnATTTTAA AATTATTCGA ACCATTATTT ACAGCAGCAG ATGGGATGGA	240
TTGGTGTAC AATTATCCTT GGnGGCCTTT GCATATTCG GGTGTAGGG AATCAGGTCC	300
GTCAATGTAG AGCCAGCAAT TGCAGCCATT ACATATGCGA TATCGGAGCG GACTTCAAGT	360
TGCCTCAGCG GAGGACACGC	380

(2) INFORMATION FOR SEQ ID NO: 4316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4316:

GCTCTAGGAT GACTGATTGA ATGTCCATGA ATGAACAACC CCTTTGTTTA ATATCGAGT	60
--	----

TGGCAAATTT ACGTTTATCA GCGTTTCTAT GATCAGTACT TCTACGGGTA GCGTTTCTAT	120
GTAATTTACA TCATCTTAAC ATATAAATAC TTCGCTATTT AATTGAAAAC ATATCCTATT	180
ATTCTTTGTC CGTTCTGACG TTTAATATCT AGCCTTAGGC ATTTCACTTG TTAATGAATT	240
TAACTTTCTT CCAC T AACCG TCCCTAAACC CAATCCCGCA ACAGTTTTTA ACTTTTTTCGT	300
TGTTGTCCTG ACATCTCATT AAGAAAGTTT ATTCTGCTTA AA A CTTATAA TCCACACCCT	360
GAGCAAACGn TnCTTATGAC AGAGTATTAA AATAAGCCGn	400

(2) INFORMATION FOR SEQ ID NO: 4317:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4317:

CCTTATTGAT AATGGTATGA GAATATTTGT TCGA A TGGA TGAAGGTAAT GAGTGAGAAA	60
CTGGATTTTT AAAGTATGAG ACAATATTTT AAAAAGTTCA ATTATTAACT TATAAGCAAA	120
TAATTGCTAT AAAAAAGTTT GGACGTGTAC AATTGCAATA TGAAGATTTT AAATTAATTG	180
TAAAGTATCG TGGAGTGGGT AACGTGTCAG AACATGTATA TAATCTTGTG AAAAAGCATC	240
ATTCTGTTAG AAAATTTAAG AATAAACCTT TAAGTGAAGA CGTTGTTAGG AAATTGGTAG	300
GAGCTGGGCA AAGCGCTTCG ACGTCAAGTT TCCTGCCAGC ATACTCCATT ATTGGTTCGG	360
CGGTGGGAGG TTAAnGGAAT TTACGGGGAG GTTCTGGGCA	400

(2) INFORMATION FOR SEQ ID NO: 4318:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4318:

TAACTACGTC TCCTGTTTCT GGATTCTTAA TTCCTGGTTT ACCTGGAACT TCCTCTTTCT	60
CTCCTGTTGG TAACTTCGGA TCAAATTCGT CTCGATGACC TGGTGTTATC GTTTCTGGTC	120
CGTATTCTGT TAATTCATTA ATCGGATCTn TTGTGATTTC TTCTTTCGAT TCACCTGTAC	180
TAATAATTTT TCCAGTTAAT GGATTTTTTA GTGTTG C GT CGTTATTGTC TTCTCACCTn	240
TTTGTCTTTC TCTTGTA A CT TTTTCTGTCC CGGTGCTAAA TnCGGATTAA ATTACGGTCT	300
TTCTTGAAGG AATCTCTTC	319

(2) INFORMATION FOR SEQ ID NO: 4319:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4319:

AGGTGCATTG AGAGAATTTG TAAATGACGT ATTAGGACCT CAAGACGATA TTACTAATT	60
TGAATACTTA AAAAAATCTT CTCAAATAC AGGTACTGTC AATTATTGGT ATTCAACTTA	120
AAGATCATGA TGATTTAATA CAACTCAAAC AACGTGTnAA ATCATTTCGA TCCTTCCAAT	180
ATTTATATTA ATGAAAATAA GATGTTATAT TCATTGTAA TTTAACACAT AGTAAGAAAA	240
ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC TGCTTTTTTAT TATACTTTAC	300
ATTTGCTCGT TTCGTCAGAT TGCAAACGTT TTCACTTCGC CAAGCCCATC TTTCnTTGGn	360
GTTTGCCT	368

(2) INFORMATION FOR SEQ ID NO: 4320:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4320:

TAAGTTAGCT ACCATCCTCG CTAAGAACCT TTGTGACTT GTGACAATCG CTTGCTTCTT	60
TCCTCTCCTT CGGCTCTCGC TTAATCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT	120
CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT	180
TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTCACGGT CTCAACTTGC CTGGCAACE	240
TCTACTCTAG CGGAAnTAA GTTGGnCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT	300
GACAATCGCT TGCTTCTTTT CCTCTCCTnC GGCTCTCGGT TAACTCA	347

(2) INFORMATION FOR SEQ ID NO: 4321:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4321:

```
GGGCAAGTTA CAGTGGTGCA TGGTTGTCGT CACTCGTGTC GTGAGATGTT GGGTTAAGTC      60
CCnCAACGAG CGGCAACCCCT TAAGCTTAGT TGCCATCATT AAGTTGGGCA CTCTAAGTTG      120
ACTGCCGGTG ACAAACCGTA GGAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA      180
TTTGGcTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGC GAGTCaAGCA      240
AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGtTGCA ACTCGaCTaC ATGaAGCTGG      300
aATCGCTaGT aATCgTGGTC CAGCATGCTA CGGT      334
```

(2) INFORMATION FOR SEQ ID NO: 4322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4322:

```
CTGTTAAACG ACTACAGGAA GTATTTACAA TCAAATAAG CAAAAGTATT CAGATGCCTC      60
AGATAAAGCT TGGGCGCATT CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTtAGCAA      120
CGATATAAAA GTGCAAAGGG TTGGCTAATA GATATGGCTA ATAAATCGCG CTCGAAATGG      180
GATAATATTT CTAGTACAGC ATGGTCAAT GCAAAATCCG TTTGGAAnGG AGCATCGAAA      240
TGGTTTAGTA nCTCATTACA AnTCTTTAAA GGGTTGGACT GGGGATATGT ATTCAGAGCC      300
CACGATCGTT TTGATGCATT TCAGTTCGGC      330
```

(2) INFORMATION FOR SEQ ID NO: 4323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4323:

```
CAATGATGCC ATGAGCAGTG CCTCCTTTAA TAGCATTTTA GCACTGTTTT GTCGTATTTT      60
TAAATATAAA TTTGGAATGA ATAATAAAGT AGTGATTAAA TTAAGTTGTG TGATAGGAAA      120
CTTGGACATC AATCAAAGTA ATAGGCACTA aACGCTTAT TGGCGGGGCC CCAACAAAGA      180
AGCTGACGAA AAGTCACTTG CAATAATGTG CAAGTCnGGG ATGGGCCCCA ACATAGAGAA      240
ATTGGGTCCG nAATTTCTAC AGACAATGCC AGTTGGCGGG GCCCCACAT AGAGAATTTT      300
GAAAAGGAAT TCTACCAGCA ATGCCAGTTG GGGGAnG      337
```

(2) INFORMATION FOR SEQ ID NO: 4324:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4324:

```
TTACTTACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG ACTATAGCAA      60
GGAGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG TCGATGGTAG      120
TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCCAGGCA AAAAATGGAT GCGATGAGCC      180
GCATTGAGAC CGCAAGnTCT TTTTTTTATG TCTAAAACGT CAAAATAAAA AGCAAACACA      240
AAGAAAAATG GCTTGCGCAA GTGAAAACGT TTGAATCTGC CGAACGAGAA AGAGCGnACC      300
GAGTTTAGTA GAnTAAATGA GTAAGCGAGA      330
```

(2) INFORMATION FOR SEQ ID NO: 4325:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4325:

```
TTCATCCGCT CACTTTTCAA CGTAATCgT TCGGTCCTCC ATTCAGTGTT ACCTGAACTT      60
CAACCTGACC AAGGGTAGAT CACCTGGTTT CnGGTCTACG ACAAATACTA AACGCCCTAT      120
TCAGACTCGC TTTCGCTACG GCTCCACATT TACTGCTTAA CCTTGACATC AAATCGTAAC      180
TCGCCGGTTC ATTCTACAAA AGGCACGCCA TCACCCATTA ACGGGCTCTG ACgCTTGTA      240
AGCACACGGT TTCAGGTTTCG ATTTCACTCC CCTTCCGGGG TGGCTTTTCA nCTTTCCCTC      300
ACGGnACTGG TTCAC      315
```

(2) INFORMATION FOR SEQ ID NO: 4326:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4326:

TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT TAnATGCGGC TCATCGCATC	60
CACTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGAACTAC CATCGACGCT	120
AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC TATAGTCACC	180
AGACATATGA ATGTAAATTA TACATTCAAA ACTAGATAGT AAGTAAAAGT GTTTTGCTTC	240
GCAAAACCAT TTATTTTGAT TAAGTCTTCG ATCGnTTAGT ATTCGTCAAC TCCACATGTC	300
ACCATGCTT	309

(2) INFORMATION FOR SEQ ID NO: 4327:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4327:

AAAGCTTATA AACGCTCATC TGACATTGTA GAATTCATGC TTTCAAAGA CGATATACTA	60
CGACACTCCT ACGAACTTGT CCAAGGATTA CGAAAAGACC TAAGGTTATGTAATnGCCT	120
AAATTTATTA ATCGTTTAAA TTCAGTTAGT AAAAAGTCTG TGAGTAAGGG TGTATGGAAA	180
GTGGTTAAAT ATTATAGAAA ACATCAAAGG ATGTTAAGAA ATACAATTTA TTACCCAGCA	240
TTTAATAATG GTGCTATAGA AGGAATTAAT AATAAGATnA AATTAATCAA GTGAATTTCT	300
TTTGGTTnCA G	311

(2) INFORMATION FOR SEQ ID NO: 4328:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4328:

TAGCTTCTGC GAGCTAGCGG AATCGAAGCC CCAGTAAACG GCGGCCGTAA CTATAACGGT	60
CCTAAGGTAG CGAAATTCCT TGTCGGGTAA GTTCCGACCC GCACGAAAGG CGTAACGATT	120
TGGGCACTGT CTCAACGAGA GACTCnETGA AATCATAGTA CCTGTGAAGA TGCAGGTTAC	180
CCGCGACAGG ACGGAAAGAC CCCGTGGAGC TTTACTGTAG CCTGATATTG AAATTCGGCA	240
CAGCTTGTA AGGATAGTAG GAGCTTTGAA ACGTGAGCGC TACTTACGTG GAGGCGCTGG	300
TGGGATACTA CCCTAGCTGT TTTGGTnTCT nACCCGACCA	340

(2) INFORMATION FOR SEQ ID NO: 4329:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4329:

AATCCATAGC GAAATGTATA CCATCACCCA TGCGTCCTTC TAAAGGTAAA TCTCTACCTT	60
TTTGTGCACC AGTACATAAT ATAATGGCAT CATACTCAGA TTCTAACGTT GCTTTATCAA	120
TATCAACACC GACTTCAACA CCATTAATGA AAGTAATGCC CGATTCTTCC ATTAACTTAA	180
TACGACGTCG AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC	240
CGCCTGATTC TCTAGCACGT TCATAAATAG TTAAGTTCTT TCCTnGTAGA TTAAGTTCTT	300
CAGCAGCAGT AATCCTGnTG GACCG	325

(2) INFORMATION FOR SEQ ID NO: 4330:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4330:

CACTTCACCA CAGCCGCCAT GCGAGGnGCA GTAGGAATCG AACCCACACC AAAGGTTTTG	60
GAGACCTCTA TTCTACCGTT GAACTATGCC CCTATTAAAA ATAATAAATG GAGGGGGGCA	120
GATTGGAAT GCCGAACCCG AAGAGCGGAT TTACAGTCCG CCGCGTTTAA CCACTTCGCT	180
ACCCCTCCAT AAATGGTGCG GCGGnGnAGG ACTTGAAACC CCCAACCCAC TGATTACAAG	240
TCAGTTGCTC TGACCAATTG AGCTAAGGCC GGCTAAGAAA TGGTTCCAGG ACAGAGTCGA	300
AACTGCCGAC ACATGGGAGC TTTCAAT	327

(2) INFORMATION FOR SEQ ID NO: 4331:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4331:

GCATCATTTT CAGCTTCCCA CTTCCACATT TGGAAAATTT CTCCAGTAAC AATGAAAGAC	60
---	----

CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA	120
ATAATGACCA TTTCCCAAAT GCCTAAGAAA ATAATAAATG TGATAATAGG TAATATAAAT	180
TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA	240
AGTCATCATA TGCAGGTGGA TTAACAAAT GATGTTGTTT TACCAATGTC GTAATTTCTT	300
GGATAGCCGG ATGGnTTAA TGTTTAAAAT CACCATAGGG TGTCCnGCC GTGGACTGTG	360
GTTAAAAACG TCACGGACTT TGTTTAAAAn GGTGCGTCAT	400

(2) INFORMATION FOR SEQ ID NO: 4332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4332:

CTGGTATGCA GATTTACCAC CTGCCTCTCC ACAAnTnnGG GGAAGCAAA CAGATGTGCC	60
TGAATCAAGT GACTGGTATA ACGCATCATA CATTATTATG TGGGGCTCTA ATGTACCTTT	120
AACACGTACT CCGGATGCAC ATTTTATGAC TGAAGTCCGC TATAAAGGTA CAAAAGTCAT	180
TTCAGTAGCA CCAGATTACG CAGAAAATGT GAAATTTGCA GATAACTGGC TAGCACCGAA	240
TCCTGGTTCA GATGCTGCAA TTGCACAAGC AATGACGGCA TGTTATTTTA CAAGGAACAT	300
TATGTTAAAT CCAACCTGAA TGAACGGTTT TTATTAAATT ACGGTTAAAA CCATTATTAC	360
CAGGAT	366

(2) INFORMATION FOR SEQ ID NO: 4333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4333:

TATTATTTCA TTGAGCAGAA AGAAAATTAT GGCACCAAAC TTTAATATTT TTTTCAATGT	60
CATTCTTTTG AnGGGAGTGG GACAGAAATG ATATTTTCGC AAAATTTATT TCGTCGTCCC	120
ACCCCAACTT GCATTGTCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCATC	180
CCCAACTTGG CACATTATTG TGAAGCTGAC TTTTCGTAC TTGCTGGTT GGGGCCCTCA	240
CCCAACTCG CATTGCCTGT AGAATTTCTT TTCGAAATTC TCTGTGTTGG GGCCCTGGA	300
CTGAGAATTG GAAAAAGCT TGTTGACAAG CGnATTTTC GTTCCATGCA ACTGACTGCC	360

AAGAGAAcNt CGTGAGAGCn ATGAAGAAGA TTGGATTTGA

400

(2) INFORMATION FOR SEQ ID NO: 4334:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4334:

CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA ACGCGTTATT AATCTTGTGA	60
GTGTTCTTTC GAACnTATGC GATTATTTCT TATGAATTCA AGCTTATTTA AACTCTTTA	120
TTCACTCGGT TTTGCTTGGT AAAATCTATA TnTTACTTAC TTATCTAGTT TTCAATGTAC	180
AATTTCTTTT TAGTCAAGCG CTGCATAAG CAATATCACT TTAACCAAAA AATATTTGAA	240
TGTTAAATAA ACATTCAAAA CTGAATACAA TATGTCACAT TATTCGCCA TCTTCTGnAA	300
GAAGATGTT	309

(2) INFORMATION FOR SEQ ID NO: 4335:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4335:

nAGGACTTTT CTCGGTCAGT GTGAAAATCA ACGCACTCGT AACACAATG TCTTCTCCCC	60
ATCACAGCTC AGCCTTAACG AGTACCGGTA TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA	120
CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC CCCCCATCGA TTAAAACGAT	180
TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCG GnCTCAGCTT	240
AGGACCCGAC TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA	300
CGGGATTCTC ACCCGTCTTT CGCTACTCA	329

(2) INFORMATION FOR SEQ ID NO: 4336:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4336:

CAAAGTGACA GGTGGTGCAT GGTTGTCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC	60
CCGCAACGAG CGCAACCCCTT AAGCTTAGTT GCCATCATTA AGTTGGGCAC TCTAAGTTGA	120
CTGCCGGTGA CAAACCGnnn GAAGGTGGGG ATGACGTCAA ATCATCATGC CCCTTATGCA	180
TTTGGGCTAC ACACGTGCTA CAATGGGACA ATACAAAGGG CAGCGAAACC GTGAGTGCAA	240
GCAAATCCCA TTAAAGTTGT TCTCAGTTCG GATTGTAGTC TGCACTCGG ACTACATGAA	300
GCTGGAATCG	310

(2) INFORMATION FOR SEQ ID NO: 4337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4337:

CCAGCACCGG GGCAGGCGTC ACCCTCATAC ATCACCTTAC GGTTTAGCAG AGACCTGTGT	60
TTTTGATAAA CAGTCGCTTG GGCCTATTCA CTGCGGCTCT TCTGGGCGTT AACCCATAAG	120
AGCACCCCTT CTCCGAAGT TACGGGGTCA TTTTGCCGAG TTCCTTAACG AGAGTTTCGT	180
CGCTCACCTT AGAATTCTCA TCTTGACTAC CTGTGTCGGT TTGCGGTACG GGCCTATTT	240
TCTATCTAGA nGGCTTTCTC GGCAGTGTGA AATCAACGAC TCGAAGACAC AnTGGCTnCT	300
CCCATCAGAG CTCAGCCTTA ACGA	324

(2) INFORMATION FOR SEQ ID NO: 4338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4338:

CGGACATCAA ACGGATGCTG CTCGATTGGC AAATGCATAT AACTAGTAAC ATGATCATCG	60
ACATCAAATT TAGATGATCA AATGTcCCCA ATcATTAATT TGATTCCGGT GTTTGCTCAA	120
TTGATTATAT GTTTTTCCTA GCACTTCATG CGGCACCATATCTTTACCTA GTAGCCACAA	180
AGATAAGTCT AACAAAGTGGC AACCATAATC GATTAACTA CCGCCACCTT GCAACGCTTT	240
ATTGGTAAAA ACACCCCAGC CAGGCACTTT ACGCCTACGC ATCGCTTGTA CACGTGCTAC	300
TAAAGGTTTA CCAACCACAC CTGATTCAAT TGCTTTTTTA GCAGTAATTG CCACATCTGT	360

GTGACGATAA TGATATGCGC CAGTAATAnT TTGTGnTTT

399

(2) INFORMATION FOR SEQ ID NO: 4339:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4339:

TGAGGCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG	60
CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC	120
CTAAGTGGAC TCGAACCACC GACCTCACGC nTATCAGGCG TCGCCTCTAA CCAGCTGAGC	180
TATAGGCCCA TTTnTTTGAA TGTTAAATAA ACATTCAAAA CTGGAATACA ATATGTGCAC	240
GTTATTCCGC ATCTTCTGAA GAAGATGTn CCGAATATAT CCTTAGAAAG GAGGTGATCC	300
AGCCGCACCT TCCGGATACG GCT	323

(2) INFORMATION FOR SEQ ID NO: 4340:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4340:

GGCTAGCCCT AAAGCTATTT CGGAGAGAAC CAGCTATTTT CAGGTTTCGAT TGGAATTTCT	60
CCGCTACCCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTTCGGTC CTCCATTCAG	120
TGTTACCTGA ACTTCAACCT GACCAAGGGT AGATCACCTG GTTTCGGGTC TACGACCAAA	180
TACTAAACGC CCTATTCAGA CTCGCTTTTCG CTACGGCTCC ACATTTACTG CTTAACCTTG	240
CATCAAATCG TAACTCGCCG GTTCATTCTT ACAAAGGCA CGCCATCACC CATTAACGGG	300
CTCTGAACTA ACTTGGTAAA GCnCCGGTTT nCnGGTCCTAA TTTT	344

(2) INFORMATION FOR SEQ ID NO: 4341:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4341:

TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGnGATAGGC GAACGTGCGA	60
TTGGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC	120
TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA	180
AAGCCTCTAG ATAGAAAATA GGTGCCCCGTA CCGCAAACG ACACAGGTAG TCAAGATGAG	240
AATTCTAAGG TGAGCGAGCG AACTCTCGTT AAGGAAC TCG GCAAATGAC CCCCATAACC	300
TTcNgggAAA AAGGgnTCCC CTTTAAGGGT TAACCGCCCC AAAAAACCCC C	351

(2) INFORMATION FOR SEQ ID NO: 4342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4342:

AATAATGACT CCTACGGGAC TCGAACCCGn GTTACCGCCG TGAAAGGGCG TGTACTTAA	60
CGTATGACCA AGGAGCCATG GCTCACCAGG TAGGACTCGA ACCTACGACC GATCGGTTAA	120
CAGCCGATAG CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC	180
TCTAGCGGAA nTAAATTCGA ACTACCATCG ACGCTAA nGA GCTTAACTTC TGTGTTCCGC	240
ATGGGAACAG GTGTACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT	300
TCAAAACTAG ATAGTAAGTA AAAGTGA	327

(2) INFORMATION FOR SEQ ID NO: 4343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4343:

ACCGCTTGGG CTGACATTTT TGGCTTGTTA AGCAGCTTGC CTACTTTTTT GGCAATAGCA	60
CCATACGTTG TTAGAGTCCC ATAAGGAACC TGTCTAATT CATTCCAAAC AACTGTTGA	120
AAATGACTAC CTGTTGGCTT TAAAGGTATT GTGATTTTCA GATTGTCACC TTTAAATAC	180
GCGTCTAACC ACTGTGTCGC CTCTCTAAAT ATCGCTAAAG ACGTATTTTC TTCCCTAGTA	240
CCATCACCTT GTTGATTTTC AAACAAAACA GCGGTCAGAC TTACCCCATC ACTCAAAAGT	300
TCCAA nCGTC CTGACAGGCG AAnCAGAGTG AACGCTGAGA CTCCAGAAAA ATCCCCCTnT	360

(2) INFORMATION FOR SEQ ID NO: 4344:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4344:

```
ATTCCGACAT CTTCTGAAGA AGATGTTnCC GAATATATCC TTAGAAAGGA GGTGATCCAG      60
CCGCACCTTC CGATACGnCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC      120
GACGGCTAGC TCCTAAAAGG TTA CTCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT      180
GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT AGCATGCTGA TCTACGATTA      240
CTAGCGATTC CAGCTTCATG TAGTCGAGTT GCAGACTACA ATCCGAACTG AGAACAACCT      300
TATGGGATTT GCT                                                              313
```

(2) INFORMATION FOR SEQ ID NO: 4345:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4345:

```
ATTTTATCGT AAGATTTTTT CGCAATGAGA TTTGGATCGT TTTTGTCCAC TACAATATCT      60
AATAGTTTTA CTTTAAGTCC AGCATTCACA AAAAGTGCTG CCAGTTGAGC GCCCATTGTG      120
CCTGCGCCAA GAACGGTTAC TTTATTAATT GTCATAGTGA TTCCTCCAAT TTAGTTAGG      180
ATAAGATAAC CATTAAGATA ATTGGAATAA CGTTGCTATT TTATAAAATT AATTAAGTAT      240
CTTTGACAGT CATCTTAGCC TCTTATTTAA GGnAAAAGCn TTATGCTTAA nATAAGTCTT      300
TTTTA                                                                      305
```

(2) INFORMATION FOR SEQ ID NO: 4346:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4346:

GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGCA AGTCTTACGG CATCTTCTAT	60
TTTTAAGCTT GAATTTAACA AATCATAAGC CGTATGAATA TTTAAATATG CCACCATGAT	120
TGAATGGnCC CTTTCTATTA GTTAAGTTTG TCGGTAAAGC TGTCAGCAAGT TGCTCAAATT	180
CATCCCCAGC TGTCCTACTGA AACTCCTGGA CGATTTCGGA TGAnCAACGC CAACCAAAAT	240
CTTGCGCAAT ATCCATTAAT AAACCAATTG CCCTTTAGAA CGTAATCGAC ATCCGGATTC	300
AnTACCTTCA TCGACTGCAA ATACCCATAA TTTCCAGCCT TGATGTCAGC AATGTAATAA	360
CCAACCTGAGA TGCTCATTGG CTGATACGAT GnTCCATACA	400

(2) INFORMATION FOR SEQ ID NO: 4347:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4347:

TCTGGGTTGA GTCGGGTCCT AAGCTGAGGC CGACACGTAG GCGATGGATA ACAGGTTGAT	60
ATTCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT	120
GGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT	180
AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA GTCGTTGATT TCACACTGGC	240
CGAGAAAAGC CTCTAGATAG AAATAnGTGC CCGTACCGCA ACCGACACAG GTAGTCCAAG	300
ATGAGATTCTn TAAGGTGGAG CGACGAATCT CCGTTAA	337

(2) INFORMATION FOR SEQ ID NO: 4348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4348:

GTAAAGACAC CGCCCTTTCA CGGCGTAACA CGGGTTCGAG TCCCGTAGAG GTCACCATT	60
TTTAGGTCTC GTAGTGTAGC GATTAACACG CCTGCCTGTC ACGCAGAGAT CGsGGGTTTCG	120
ATTCCCGTCG AGACCGTACA AATGCCTATC CAAGAGGATA GnATTTTTTT TGC GTTTAAT	180
ATTATATTAA TAAAAGATAT ATGGACGAAT GATAATCATA TTGATTTATC TGTTGTC	240
TTTTCTTTAA AATGTATGAA CCTCAAGTAA CTTAGTGGTT GGATATGAAA GATAAACGTn	300
GACAATAAAA TCTTTATT	318

(2) INFORMATION FOR SEQ ID NO: 4349:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4349:

CTTTAAAGCA CGTATAATGA TGATTTTCAG CTGTACAAA GGAGAAAAAA AGAAGACAAC	60
CAAGCCCAAT AATGGACTGG CCGCCTAATA ATAAAAGCTC TAAAAGTTGT ATTTTAAAAA	120
TAGTTCTTTA AATTATATAC CCACCACATT TGGTGnAGnA ACCTAAAAAA AnGCACTTCC	180
CAAAAATGGA AAGTGCAAGT AGTGAGCCAT AGAGGATTCG AACCTCTGAC CCTCTGATTA	240
AAAGTCAGAT GCTCTACCAA CTGAGCTAAA TGCTCTAAA TGGCTGGGCT AGCTGGGATT	300
CGAACCAACG AGTGACGGA	319

(2) INFORMATION FOR SEQ ID NO: 4350:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4350:

ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG	60
GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GTAATTCTC	120
CAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT	180
AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACCGATCGGT	240
TAACAGCCGA TAGCTCTACC ACTGnAGCTA CTGTGGATTG AATCATTATG CCTGGCAACG	300
TTCTTACTAT AGCGGAAnGT CAAGTTCCGC ATnACCATAC GAAGCT	346

(2) INFORMATION FOR SEQ ID NO: 4351:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4351:

ACGTCCTTCA TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT	60
ATGTTTCCAC CATTTTTATA AGTnAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG	120
ATTTAAACGC GTTATTAATC TTGTGAGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG	180
AATTCAAGCT TATTTAAAAC TCTTTATTCA CnCGGTTTTG CTTGGnAAAA TCTATATTTT	240
ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGA GACTAGCGGG ATCGAACCGC	300
TGACC	305

(2) INFORMATION FOR SEQ ID NO: 4352:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4352:

GTTCAATCAAT TGCTAATTCC AGTCCGCCTA ACGGATCAAT TTCATCCGCA TGTATTTTCA	60
CTTTAAAACC TGGCTTCTTT GGCTTTTTGC ATATAATGTT GCGATTGTTT TATTGTAAAT	120
ACACCTGTTT CACAGAAAAT ATCCGCAAAG TCTGCATATT GTTTTACTTC CGGAAGTAAC	180
GCAATCATTT CTTCTAAAAA TGCCTCATTT GAACTTGCCT CTTTAGGTAC AGCATGAGGC	240
CCTAGGAAAG TATGTTTCAT GTCTAAATCA TATTTCTCAG CTAAACGATT AGnCACTTTC	300
AA	302

(2) INFORMATION FOR SEQ ID NO: 4353:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4353:

TCTACCGCTG AACTACTTCT GCGGTGAAG GGAGTCGAAC CCCACGCCG TAnnTGAGGA	60
TCCTAAGTCT AGTGCGTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC CATAGAGGAT	120
TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AAtGGCTCTT	180
CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTCAGTTGCTCTA	240
CCAATTGAGC TAGGCCGGCA ATATGTAAGA ATAAATGGTG GAGAATGACG GGTTCGAACC	300
GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC CGnTTTAAAA	360
CTGCTGGCnA CGGTCTAnTC TAAGGGGACG TAAGGTCGAC TACCATCGAC G	411

(2) INFORMATION FOR SEQ ID NO: 4354:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4354:

TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTGGa	60
CGACAACCTGG TACACCAGAG GTATGTCCAT CCCGGTCTCT TCGTACTAAG GACAGCTCCT	120
CTCAAATTTTCTACGACCAC GACGGATAGG GACCGAACTG TCTCACGACG TTCTGAACCC	180
AGCTCGCGTa CCGCTTTAAT GGGCGACAG ACAAGCCCTT GGGGACCGAC TACAGCCCCA	240
GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTnCCCGT CGATGTGAAC TCTTGGGGGA	300
GATAAGnCTG TTATCCCCGG GGTAACTTTT ATCCGTTGAG CGATGGGCCC TTACCATGCG	360
GAAACCA	367

(2) INFORMATION FOR SEQ ID NO: 4355:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4355:

GTATTTTAAA TCATAGTGGT TTATGCGTCT TTTTCAAATT CTATAAAAAA TCGGATGACG	60
TGTAATCTGC CATAGATTAA CACATTCATC CGATTTATAA TAATAAGATA GACTAACATT	120
TATTGAGAGC GGGACGGAAA TGATAAAGAA CGACTAATGA TTGATTATGT AGCGATTCTT	180
TATCATTAGT CACAGCTAAT GTGTACTTAA AAATATGAAT GCATGAGTTA CACTCAnATT	240
AGAGGAAATA CTAATTTCTA AAGAAAAAGT ATTTCTTTAT GTTGGGGnCC ACCCCAACCT	300
GnCATGTGCT GTT	313

(2) INFORMATION FOR SEQ ID NO: 4356:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4356:

GGGCTGGGTT CAGAACGTCG AGCAGTTCG yTCCCTATCC GTCGTGGGCG TAGGAAATTT	60
GAGAGGAGCT GTCCTTAGTA CGAGAGGACC GGGATGGACA TACCTCTGGT GTACCATTG	120
TCGTGCCAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AGATCCTGAA	180
GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATC CTCAAAGATG	240
ATGAGGTTAA TAGGTTTCGAG GTGnGAAGCA TGGTGACAGT GGnAGCTGAC GAATACTAAT	300
CGATCGAGGA CTTAATCAAA ATAAATGTTT TGC GA	335

(2) INFORMATION FOR SEQ ID NO: 4357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4357:

GCTCTAAAAG TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTTGGTGn	60
nGAACCTAAA AAAAAGCACT TCCCAAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT	120
TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA	180
ATGGCTGGGC TAGCTGGATT CGAACCAACG AGTGACGGAT nAAAGTCCGT TGCCTTACCG	240
CTTGGCTATA GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCCGA	300
AGAG	304

(2) INFORMATION FOR SEQ ID NO: 4358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4358:

ATAATGGTGA CGTTGATGAT GCATTAACAC AAGGTAAAGC AGCAATTGAT GCTATTCAAG	60
TAGATGCTAC TGTTAAACCT AAAGCGAACC AAGCTATTGA AGTAAAGCA GAAGATACGA	120
AAGAATCTAT TGATCAAAGT GACCAGTTAA CTGCTGAAGA AAAAAGTGA GCATTAGCAA	180
TGATTAAACA AATTACAGAT CAAGCTAAAC AAGGTATTAC TGATGCAACA ACAACTGCTG	240
AAGTTGAAAA AGCGAAACTC AAGGACTTGA AGCATTTGAT AACATTCAAn TCGACTCAnC	300
AG	302

(2) INFORMATION FOR SEQ ID NO: 4359:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4359:

```
GGTTGGGAAA TCATTGCATG AGAGTGTGAA AGGGCATAAG GGGAGCTTGG ACTGCGAGAC      60
CTACAAGTCG AGCAGGGTCG AAAGAGGACT TAGTGATCCG GTGGTTCCGC ATGGAAGGGC      120
CATCGCTCAA CGGATAAAAG CTACCCCGGG GATAACAGGC TTATCTCCCC CAAGAGTTCA      180
CATCGACGGG GAAGTTTGGC ACCTCGATGT CGGCTCATCG CATCCTGGGG CTGTAGTCGG      240
TCCCAAGGGT TGGGCTGTTT GCCCATTAAG GCGGTACAnG GCTGGGTTCA GAACGTCGTn      300
AGAAAGTTCG GTCCCTATCC GTCCTGGGGC GTAGGAAATT TnGAGAGAG      350
```

(2) INFORMATION FOR SEQ ID NO: 4360:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4360:

```
AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC      60
GGTGTGTACA AGACCCGGGA ACGTATTACG CGTAGCATGC TGATCTACGA TTACTAGCGA      120
TTCCAGCTTC ATGTAGTCGA GTTGACAGCT CACAATCCGA ACTGAGAACA ACTTTATGGG      180
ATTTGCTTGC ACCTCGnGGT TTCGCTGTCC CTTTGTATTG TCCATTGTCA GCACGTGTGT      240
AGCCCAAATC ATAAGGGGCA TGATGATTTG GACGTTTCATC CCCAnCTTCC TCCGGnTTGT      300
ACACCGGCAG TTCAACTTAG AGTGCCCAA      329
```

(2) INFORMATION FOR SEQ ID NO: 4361:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 424 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4361:

AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA CTCTAGCGGA	60
ACGTAAGTTG GCTACCATCG TCGCTAAAGA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT	120
CTnTCCTCTC CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGCCTCTTT	180
TCTCGTTTCG TCAGATTCAA ACGTTTTTCA TnCGnCAAGC CTTTTTCTT TGTGTTTACT	240
TTTTATTTTG ACGTTTTAGG CATAAAAAAA wGAGAcCTTG CGGTCTCAAT GCGGCTCATC	300
GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG GCTAACAACG	360
TCGCCAAAGA CCTTTCTTGA CTTGTGACAA TCGGCTTGCT TCTTTCCTCT CCTTCGGCTC	420
TCGC	424

(2) INFORMATION FOR SEQ ID NO: 4362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4362:

CACAACAAGT ATCTAAGATA CTGGCCGAAG ATTGTCACAG ACGGTAGGGG AAGGGGGTCA	60
CGTGTACGAC CCAACATGTG GTTCCGGTTC ATnGTTGTTA CGTGTGTTGTA AAGAAACGCA	120
ATTnAnTCGT TATTTCCGGC AAGAACGTAA CAATACTACA TACAACCTAG CACCATGAAT	180
ATGTTATTAC ATGATGTGCG TTATGAGAAC TTCGAGATCC GTAATGATGA CACATTGGAA	240
AATCCAGCCT TTTTAGGCAA TACATTTGAT GCGGTTATTG CGAACCATAC AGTGCGAAAT	300
TGGACAGCAG ATTCCA	316

(2) INFORMATION FOR SEQ ID NO: 4363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4363:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT	60
CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCGG AAATCTCTGG ATCAAAGCTT	120
ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA	180
AGGCATCCAC CGTGCGCCCT TGAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG	240
TTGATTAATC TTGTGGAGTG TTCTTTTCGAA CATAGCGATT ATnTCTTATG GAATTCAAGC	300

nTATTTAAAA CnCTTTGA

318

(2) INFORMATION FOR SEQ ID NO: 4364:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4364:

nTGCACTTAA GAACCTAGAC GATCGTGGTA TCGTTTATAT TGGTGCAGAA GTAAAAGATG	60
GAGATATTTT AGTTGGTAAA GTAACGCCTA AAGGTGTACT GCAGTTAACT GCCGAAGAnA	120
GATTGTCACA TGCAATCTTT GGGTGAAAAA GCACGTGAAG TTAGAGnATA CTTCATTACG	180
TGTACCTCAC GGCGCTGGCG GGTATCGTTC TTGCATGTTAAAAGTATTCC AATCGTGCAA	240
GAAGGGCGAC GATACATTAT CCACCTGGTG TTAAACCAAT TTAGTACGT GGTATATATC	300
GTTCCAAAAA CGT	313

(2) INFORMATION FOR SEQ ID NO: 4365:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4365:

AACCATTCTGA TGCAATAGCG TCATTCTTGG ATATTAATCC CTAAATTGCC GTGATATCCC	60
GCGTCTATCT TGGCCTGTTT CAATCACTAA ATGCGTTTTA CTACTTACAC CACTACGGGC	120
TAGTTAATAG TCCGACATAG CCCTCTGGTA TGCTTACAGC TACATCTGTn TTAATCACTG	180
CCTTTTCTTG TGGCTCAAGT ACGACAGTTC AGCTGAGAAT ATGTCATAAC CTGCATCCGn	240
CTTATGATTT CGTTCGGGCA TTCTAGCATT TTCTGATAAT AGCCTTACTT GTAATGTGTn	300
AGTCATTTTC	310

(2) INFORMATION FOR SEQ ID NO: 4366:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4366:

AGTGGTACTT CTGTTAATTG GTGAATTTGG ATACTGGTTA TATTCAGCTG CACCGCAAGC	60
AACTTCTATT GATGGCCTAA CTGCCTTTTT ACCTCAÆCA ATGGGTATGG TAATTGTTGC	120
AGTCATTTAT GGCTTTATGA ATATGAAAGC AGAGAATCCA TTCCGTAATA AAATTACGTG	180
GTTACAAATT ATTTTCAGGT TCTTCTTTGC ATTTGGTGCT TTAACATATC TTATTTTCAGC	240
ACAACCTAAT ATGAATGGTT TAGCACTGGA TTTATCCTTC TCAACATCCG TGGTGCTGCT	300
ACATTAA _n GG TATTAATTCT TAAACCACAT AAACGTCAAA GAATGGTAAT ACAATCACGG	360
CTAGTACCAT TTAGTAGCCG CTCCGTACCG nAATTATAAA	400

(2) INFORMATION FOR SEQ ID NO: 4367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4367:

CACCTGGACG AAACGGTTTT AGATCGTATT CAATTGAAAA GGCCGGTATT GAATGAATCA	60
CACTTAGCAG CGATTGATCA GGAACATTTT AAATTAACCT ATTTATCAAC GGTATATGAA	120
GGGGATTTGG AAGATGCGTT AGAAGCATTG TGCCGAGAAG CAGTGAATGC TGTAACAAG	180
GCGCTCAAAT TCTAGTGTTA GATGATAGTG GATTAGTTGA TAGCAATGGC TTTGCAATGC	240
CGATGTTACT CGC _n ATAAGT CATGTGCATC AATTACTT _n TAAAGCAGAT TACG _n ATG _n C	300
TACAAATTTA ATCGCTAAAT CTGGTG	326

(2) INFORMATION FOR SEQ ID NO: 4368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4368:

ATTATAGCCG AAATGCCCAA AATAGATTTT GACGAATATT ACGAATGGTT GCTTTACTTG	60
CATAAATGGC TTTAGGAATA AGCATCAAGT CGCCACCAAG AATAGTAATA TCAGCTGCT	120
CAATGGCAAC TTCTGTACCT GTAnCAATGG CGATACCGAT ATCAGCTTTA ACTAATGCAG	180
GTGCATCATT TACACCGTCA CCA _n CCATCG CAACCTTCTT ACCTTGTTGC TGTAGTTTCG	240
CAATTTGTGC AGCTTTTTCT nCTGGTAGAA TATCTGCAAT AACAGTATCT ATGCCTACTT	300

GTTTTGC

307

(2) INFORMATION FOR SEQ ID NO: 4369:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4369:

TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCAC CGGGTGTGCC TTCTGATATG	60
CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT	120
CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGATATC GTCGTTAGTA ACGTCCTTCA	180
TCGGCTTCTA GTGCCAAGc ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT	240
CCTACAGGAA ACGCGTTATT AATCTTGTGA GTGTTCTTTC GAACAYTAGC GATTATTTCT	300
TATGAATTCA AGCTTATTTA AAACCTCTTA TTCAATCGGT TTTGCTTGGG TAAAATCCTA	360
TATTTTACnT ACCnTATCGA GTTTTCAATG TAACAA	396

(2) INFORMATION FOR SEQ ID NO: 4370:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4370:

CAGTAAGATA ATTTTCAATT AGAAAATATC TTAAGTCTGT TCTCTATTTA TACAATACTT	60
CGTATTGAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT	120
GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACA TGTAATTTTA CTTTACATA	180
CTTTTAAAAA ATAAGACACT TTGCCAAACT TGCACATAAA TGTTTAATTC AATAATTGA	240
ATTTTCTGTG TTGGGTCCCT TCGTATAATT TAATAAATAC CACTAAACTA AaTTArTGAA	300
GTGCCTTATG TATAA	315

(2) INFORMATION FOR SEQ ID NO: 4371:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4371:

GTCGTCAAAT GTACCTTCAC CAAGTAGTGA TGTACATATT TACCGCCTTG TTCAACAGCA	60
CGTGTCGGCG CACCTGTAAT CGCAATGACA GGTATGCGTT CAnATATGAA CCTGCGATAC	120
CGTTGACGGC ACTTAATTCTG CCAACACCAA ATGTAGTAAC TAATGCAGCG AGTCCATAA	180
GACGGGCATA ACCGTCCGCT GCGTAACTTG CGTTTAATTC ATTTGTATTT CCTACCCAAT	240
CTACAATGGG GTTGCTGATA ATATCGTCTA GAAAAGCGAG ATTAAAATCA CCAGGGnCAC	300
CAAAATTTTT ATCGACGGCn TG	322

(2) INFORMATION FOR SEQ ID NO: 4372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4372:

CCTAAGTCTA GTGCGTCTGC CAATTCCGCC ACACCCGCAA ATGGTGAGCC ATAGAGGATT	60
CGAACCTCTG ACCCTCTGAT TAAAnAGTCAG ATGCTCTACC AACTGAGCnA ATGGCTCTTC	120
CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA GTTTGCTCTA	180
CCAATTGAGC TAGGCCGGCA ATATGTAAAG AA^AATGGT GGGAGAATGA CGGGTTCGnA	240
ACGGCGGAAC CCTCTGCTTG TAAAGCAGAT GCTCTCCAGC TTGAGCTAAA TCTCCGATTT	300
AAAAGTCTG GGCAAGTTCT ACTCTAG	327

(2) INFORMATION FOR SEQ ID NO: 4373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4373:

CATTTTAATT TATTGTACAG AACGAAATGT GATGTTAGTA GATCATAGGG TTATGATAA	60
TATTAAAGCT GAAAACGTTA TATTTATTGG CCTTTTGTGT AAACATGGAC ATTGGCATGC	120
AGTCATTTAT GACATTGCTC AAGACAAAAC TGCCGAACTC GAAATTGAAA ATATTATAGA	180
TATTTCTGAT TCATTCGGTA AGACGATTCA AACCAGAGAC ATATCCATTG ATAAGTATCA	240
TCAATTTTTTA AACCCCATCG ATTCCTAAAA AACAGCAGTA AGATGATTTT CAATTAGAAA	300

ATATCTTGCT GCTGTTCTCT ATTTATACAA TACTTCGTAT TGAATGGCTC GCTTTCCCAG 360
GGnGCCGCTC AGCCTGGGCC TCGACTGGCA ATGCTCCCTC 400

(2) INFORMATION FOR SEQ ID NO: 4374:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4374:

TAATGGATTT TTTAGTGTTG GTGTCGTTAT TGTCTTCTCA CCTTTTGTG CTTCTCTTGT 60
TACTTTTTCT GTCCCTGGTG CTAAATCAGG ATTAAATTTA CGTTCTTCT CGAATGGAAT 120
CTCTTCTTTT TCTACAATCG AGTCTCCTTT TACAGGTCCA TATTTTGTTA CGCTATCGAC 180
CGGTGGTCTA ACTACATCTC CTGTTTCTGG ATTCTTAATT CCTGGTTTAC CTGGCACTT 240
CCTCTTTCTC TCCTGTTGGT AACTTCGGGA TCAAATTCGT CTCGATGGAC CTGGTGTTGA 300
nCGTTTCTGG GTCCGnAAGT CTGTnGAATT GCAG 334

(2) INFORMATION FOR SEQ ID NO: 4375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4375:

ATACATGCAA GTCGAGCGAA CGGACGAGAA GCTTGCTTnG TGAATGTTAG CGGCGGACGG 60
GTGAGTAACA CTGGATAACC TACCTATAAG ACTGGGATAA CTTGCGGAAA CCGnAGCTAA 120
TACCGGATAA TATTTTGAAC CGCATGGTnA AAGCTTGCAA AGACGGTCTT GCTGTCACTT 180
ATAGATGGAT CCGCGCTGCA TTAGCTAGTT GGTAAGGTAA CGGCTTACCA AGGCAACGAT 240
GCATAGCCGA CCTGAGAGGG TGATCGGCCA ACTGGAACT GAGACACGGT CCAGACTCCT 300
ACGGG 305

(2) INFORMATION FOR SEQ ID NO: 4376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4376:

GATAAAGTGA AAGAACTCGG ACGTGACACC TATTGCACGA TTCGTTGGTT TTAAGGCAGT	60
AGGCGTTGAC CCGAAAATTA TGGGTATTGG GCCTGGCATA TGCATTTCCT AAGTATTGT	120
CACTCAGCAA TCTATCTGTT GAAGACATTG ATTTGATCGA ATTGAACGAn CATTTGCTCT	180
CAAACGATTG CATCTATTAA AGAAGTAGGT CTAGATATAT CACGTACGAA TGTGAATGnT	240
GGCGCTATTG CTTTAGGTCA TCCATTAGGT GCTACAGGCG CAATGTTAAC CGCGCGTTTA	300
CTTAA	305

(2) INFORMATION FOR SEQ ID NO: 4377:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4377:

AATGTCTTCT ACCCCATCAC AGCTCAGCCT TGAACGAGTA CCGGGTTTGn CCTAATACTC	60
AGACCTTGAC TGCTTAGACG TGACAATCCA ATACGACACG CTTCGCCTAT CCTACTGCGT	120
CCCCCATCG ATTAAAACGA TTATAGGTG TACAGGAAAT ATCAACCTGT TATCCATCGC	180
CTACGCCTGT CGGCCTCAGC TTAGGACCCG ACTAACCAG AGCGGACGAG CCTTCCTCTG	240
GAAACCTTAG TCAATCGGTG GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT	300
TCTCACTTCT AAGCGCTCCA CATG	324

(2) INFORMATION FOR SEQ ID NO: 4378:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4378:

CATCATGCTT AGAAAACGCT TAATTTAGGT TTTGACTTTT TAATCAGAGT ATATAAGCAA	60
AACTTATCAT ACAGGTAAGG TGTAATAAGT ATTTTTTATT AATTGAGAAT AATTATCAAT	120
TTCGCGAATG ATTCAATTCA ATTTTAAAC GTATTATTTT ATTGAGCAGA AAGAAAATTA	180
TGGCACCAAA CTTTAATATT TTTTTCATG TCATTCTTTT GATGGGAGTG GGACAGAAAT	240
GATATTTTCG CAAAATTTAT TTCGTCTGCC CACCCCAACT TGCATTGTCT GTAGAAATTG	300

GGGAATCCCA ATTCTCCTT GGTGGGGGCC CATCCCCACC TTGCACATAA TGGnAGCnGG 360
 ACCTTTCCGC CGCTCCGGGG TGGGGGCCTCnACCCCAhTC 400

(2) INFORMATION FOR SEQ ID NO: 4379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4379:

ATAAAATATA TCACTTGAAA AATTTTCATGT AGAAAAGATG ATGGATAGGC TATAAAGTAA 60
 TTGTGACTGA GATGAAC TTT TATGTCTTAG AACTACAAC ACTATATTGG CAGTAGTTGA 120
 CTGCGGGGCC CCAACATAGA GCAAATTGGA TTCCCAATTT CTACAGACAATGCAAGTTGG 180
 GGTGGGCCCC AACATGAAAG AAATACTTTT TCTTTAGAAA TTAGTATTTT TTATGCATGA 240
 GTGTACTCAT GTTGCGATTA TTTTnAGTA CACATTAGCT GTGGACTAAT GATAAAGGnn 300
 TCGCTACATA ATCCATCCAT TAGGTCGTTC CTTGATTCAT TCCCT 345

(2) INFORMATION FOR SEQ ID NO: 4380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4380:

CTAAAGCTGn CATATGCGGC TTGCCGATGA AGCCAACCCT GCTGCTGTTG GTACAAAATT 60
 GTCGCTTTCA ATTTCTGCAT ACCAATCGAT GCCAGCTCTA TTTCTGACAA TATCCATATA 120
 TTTTGAAATT TTCTCTAATT CTTTGCCACT AACCTTTTCA CCATTCAACC AAAATTGATC 180
 CTGTGTTAAC TGGTCGTAA AAGTGACTTT CGTTTCAGTG TAAAATTTTT CTAATGTAAC 240
 AGATATGCTA TTATTCATGG AAGATTAGTG CTTTCATCTTT TTTACCCCAA TATTTTATAA 300
 GTGCAATATC GTAGTGCAGG CTTGCCACTT TAACACGCAT AACTCCTAAA TCTCAACCAG 360
 ATn 363

(2) INFORMATION FOR SEQ ID NO: 4381:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4381:

ACCTGAATGA CTCAA	ACTTG	ACTTTnCGAC	AATTGACTGT	nCATTTTGCA	TAGTTGTATG	60
nCTCCATTnC	GTAATTATTA	GATTTGTTCG	CTTACGTCTA	TTGAATCATA	CAGCTTTATT	120
ATAGTTAGCG	TATTTGCACC	TTTGACATT	AAACCATGTT	TAATAATCAT	TGAATCATT	180
TTAAGTAAAT	TAAGGAATCT	ATAATGTTCG	TTAAATAAAA	CTGATCCCGT	TGTGGCTTCA	240
CACCCGATAG	ATAGGGATTT	ACAGATAAAT	TCAGGTCTCT	TCCACGTCCA	TATTTGGGAC	300
CCATCGAAAA	TCGGGTTCCTC	AAATCATCGA	ACATAACAAA	AGAAGCTAAG	CAACAGTAGG	360
GCCGTTGTCA	CTTA	ACTTCT	GTTTTTCGA	TGACAGCTTC		400

(2) INFORMATION FOR SEQ ID NO: 4382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4382:

GnACTACAAA	GCAATGGGGT	TTGCCAGTTT	CTTTATTTAC	TGACGAATAC	TGGCAATGAC	60
ATCAGATACA	TGTGGCAnCA	CCAATCCATT	TCTTTTCACC	ATTGATAACC	CAAGTATCGC	120
CTTGGGTTGC	AGGGACTGTT	TCAAGACCTC	CCGCAACGTC	CGAACCGGT	TCTGGTTCAG	180
TTAAAGCAAA	GCATGTTACG	CnTTCATGTG	AACTGTAATT	TAGGTACATA	TTTCGCAATT	240
TGTTCTTTGC	TACCTCCGAA	ATAGAAAGTG	TTATGCCCTA	AACCTTGGTG	AACACCGAGT	300
AGGG						304

(2) INFORMATION FOR SEQ ID NO: 4383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4383:

GTGCATTATT	TTGAGAATT	AGCTCAGCTG	GGAGAGCATC	TGCCTTACAA	GCAGAGGGTC	60
GGCGGTTCGA	ACCCGTCATT	CTCCACCAT	TTGATTATTA	AATTATATGA	ATAAGCTGGA	120
GGGGTAGCGA	ATGGCTAAAC	GCGGCGGACT	GTAAATCCGC	TCCTTCGGGT	TCGGCAGTTC	180

GAATCTGCCC CCCTCCACCA TCTATATATT GGGCTATAnC CAAGCGGTAA GGCAACGGAC	240
TTTGACTCCG TCACTCGTTG GTTCGAATCC AnCTAGCCCA GCCATTAGAG nCATTAACTC	300
AGTTGGTA	308

(2) INFORMATION FOR SEQ ID NO: 4384:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4384:

AATTTTGGCC AAAACACCCA TCCGCTGTAA CTTCAGAGTG TCATGGCAT TTATTACACT	60
ATCTCCAACT CCTAGTGGAA CAACCACATC TCGTCCTTGG GGTGCATGGA ATGTTCCGTC	120
AGCCCTGTGA ATTATTTCTT GAACTCCACC ACCTGGGGCG TTTCCAGAAC CTCTATCATT	180
TAATACAGCA AATGTCGGTT GCGTTAATGC TCCTGAATTA TCGGKAGCTA CACCCTTTCC	240
TGCTAAAGTA CCAGTAGACA ATGTAGGTAT TGGCTTGATG AGATTTtTAT CAGTAATGGC	300
TTTAGAnAT	309

(2) INFORMATION FOR SEQ ID NO: 4385:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 basepairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4385:

AAAGGTGAAA AGCACCCCGG AAGGnAGGTG AAATAGAACC TGAAACCGTG TGCTTACAAG	60
TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG GCGAGTTACG	120
ATTTGATGCA AGGTTAAGCA GTAAATGTGG AGCCGTAGCA nAACAGGTCT GAATAGGGCG	180
TTTAGTATTT GGTCTAGACC GAnAACCAGG TGATCTACCC TTGGTCAGGT TGAATTCAGT	240
AACACTGAAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGtTGA ACTGAAGGTA	300
GCGGAGAA	308

(2) INFORMATION FOR SEQ ID NO: 4386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4386:

TAGAATCTTC ATCAATATGA TCTAACCAAT ATTGATAAAA CCTTGATGTG TTTCTGTGTC	60
ATGACATACC ATATCGACTA GGTACCTTTT TAGAATGTTG ATTAATCAnG GCAAATATCA	120
TGGCAAGGTC ATCTTCAAAA TGATTCGATT CAAGTGGAAG GCATATGACG TCTCATCACT	180
ATACCCTTTT TCCCATTCTG CAAATCCACC ATAAATACTA CGCGACGCGG AACCCGGACC	240
CATTGCGGGC AATCTCGGTn AATCCTTATC TGGACAGCTG GCATGTCTAG CGGCTGGATT	300
TACAAGCTGG CTGGCTAAAG CTGGCATATG CGCTTGCCGG TTGAAGCCCA ACCTGGCTGG	360
CTGGTGGGGn ACAAATTGGT CGCTTTTCAA TTTCTnGGCAT	400

(2) INFORMATION FOR SEQ ID NO: 4387:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4387:

TCAATTTATG GGGCATTATG ACTTTATATA CCTAAAATAC TATTAAGAAG TCCTGAAAAA	60
TTACATTAG CAGTTGGATT GTTCAACTTT ATTAATGATA AGATGCAA TAATTTTACA	120
GTGTTTGCAG CAGGGGCAAT TATGATTGCA GTACCTATAG CAATCGTATT CTTGTTCTTG	180
CAACGCTATT TAGTATCAGG TTTAACAACA GGTGCGACAA AAGGTTAGTT TGAAATTCnC	240
GnGTGGGGCA GAATTGATAA AGAACCACnA ATGACGATAA AGATTAAAAG GAGGACGTTA	300
TGGATGACGA	310

(2) INFORMATION FOR SEQ ID NO: 4388:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4388:

AACATCATGC TGATGTTGTT GAATATGAAG AAGATACAAA CCCAGGTGGT GGTCAGGTTA	60
CTACTGAGTC TAACCTAGTT GAATTTGACG AGATTCTACA AAAGGTATTG TAACTGGTGC	120
TGTTAGCGAT nCATACAAcA ATTGAAGATA CGAAAGAATA TACGACTGAA GTAATCTGAT	180

TGAACTAGTA GATGAACTAC CTGAGGAACA TGGTCAAGCG CAAGGACCCA TTCGAGGAAA	240
TTACTGGAAA ACATCATCAT ATTTCTCATC nGGTTTAGGn ACTGAAATGG TCACGGTAAT	300
TTTGGCGTGG	310

(2) INFORMATION FOR SEQ ID NO: 4389:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 302 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4389:

TTTACCATAT CATCCACTAT TTATTAAACC TAATAAAGAT GAATTAGAAG TGATGTTTAA	60
TACAACAGTG AACTCAGACA CAGATGTTAT TAAATATGGT CGTTTGTTAG TTGATAAAGG	120
TGCGCAATCT GTTATTGTCT CGCTTGGCnG TGGATGGTGC TATTTATATT GATAAnGAAA	180
TCAGTATTAA AGCAGTTAAT CCACAAGGGA AAGTGGTTAA TACAGTTGGC TCTGGTGATA	240
GTACAGTTGC AGGCATGGTG GCTGGGAATT GCTTCAGGTT TAACGnTTGA AAAGGCATTC	300
CA	302

(2) INFORMATION FOR SEQ ID NO: 4390:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4390:

AAAGAGTGCG TAATAGCTCA CTAGTCGAGT GACACTGCGC CGAAAATGTA CCGGGGCTAA	60
ACATATTACC GAAGCTGTGG ATTGTCCTTT GGACAATGGT AGGAGAGCGT TCTAAGGGCG	120
TTGAAGCATG ATCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG	180
CGAAAGACGG GTGAGAATCC CGTCCACCGA TTGACTAAGGTTTCCAGAGG AAGGCTCGTC	240
CGCTCTGGGT TAGTCGGGTC CTAAGTGAGG CCCACAGCGT AGGCGTGGAT ACAGGTTGTA	300
TnCTTACCA CCTATAATCG nTTAATCGTG GGG	333

(2) INFORMATION FOR SEQ ID NO: 4391:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4391:

AGTGCGTTTG TGCACAnACT TGACTGnAAC TTAGTGCCAT TGCAGCACCA GCAACCCATG	60
GCGCAATAAG CCCAATGCAG CTATAGGGAT ACCGnCAATA TTATAGCCGA ATGCCCCAAA	120
TAGATTTTGA CGAATATTAC GAATGGTTGC TTTACTTGCA TAAATGGCTT TAGGAATAAG	180
CATCAAGTCG CCACCAAGAA TAGTAATATC AGCTGCTTCA ATGGCAACTT CTGTACCTGT	240
ACCAATGGCG ATACCGATAT CAGCTTTAAC TAATGCAGGT GCATCATTTA CACCGTCACC	300
AACCAT	306

(2) INFORMATION FOR SEQ ID NO: 4392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4392:

TACGGTATGC ATATCTTTTA AAACCTATTC TTTTGTTATT AGGACATATA AATTCATCAT	60
TAAGTTCGTC ATATTTCCAA TTTTAAGTGT TGAAAATC ACTTTTAAAC TTTCTAGTTT	120
TATCTTTAAT AAACATGCCA TACGTAATAA GTGGCGTTTT ATTAAATCA TCTATAATAG	180
CCATATAGTT TTGCTCACTA CCATAACCTG CATCAGCTAC AATATACTCC GGTAAATAAC	240
CGAAGGGATT TTGAATCATT GTTAAAAATG GAATTAAAGT TCTAGTATCT GTTGGGTTTT	300
GAATAGGGTC ATGGGATAAA CCAAATGnGG AATTGCCnC AATTnGTAAA TGGAA	355

(2) INFORMATION FOR SEQ ID NO: 4393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4393:

CATTCCGTAA TAAATTACG TGGTTACAAA TTATTCAGG TTTCTTCTTT GCATTGGTG	60
CTTTAACATA TCTTATTTCA GCACAACCTA ATATGAATGG TTTAGCAACT GGATTTATTC	120
TTTCTCAAAC ATCGTTGTG CTGCTACAT TAACTGGTAT TTATTTCTTA AAACAACATA	180
AAACGTCAAA AGAAATGGTT ATTACAATCA TCGGCTTAGT ACTCATTTTA GTAGCCGCTT	240

CTGTTACAGT ATTTATAAAA TAAGGAGTGT AGATGTCATG AAAAAATCAG CGGTTTAAAT	300
GGAACCTATT CCAAAGCCAT CGCGACCAAT GGGTCATTG GATTAnTAAC GATAATGGCG	360
nnGG	364

(2) INFORMATION FOR SEQ ID NO: 4394:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4394:

GATTAAAACG ATTATAGGTG GTACAGGAAT ATCAACCTGT TATCCATCGC CTACGCCTGT	60
CGGCCTCAGC TTAGGACCCG ACTAACCAG GAnCGGACGA GCCTTCCTCT GGAAACCTA	120
GTCAATCGGT GGACGGGATT CTCACCCGTC TTTCGCTACT CACACCGGCA TTCTCACTTC	180
TAAGCGCTCC ACATGTCCTT ACGATCATGC TTCAACGCCC TTAGAACGCT CTCCTAnCAT	240
TGTGCCAAAG GACATGCCAC AGCTTCGGTG AATATGTTTA GCCCCGGTAC ATTTTCGGCG	300
CATGTnCACT CGACT	315

(2) INFORMATION FOR SEQ ID NO: 4395:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4395:

AGCCCCCAAA TGGGTATTGA AATTGAATGG TGGGnCTGA AnTGGACTCG AACCACCGAC	60
CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT AGGCCCATTA ATTTGAATGA	120
ACAAACATTC AAAACTGAAT ACAATATGTC ACGTATTCC GCATCTTCTG AAGAAGATGT	180
TCCGAATATA TCCTTAGAAA GGAGGTGATC CAGCCGCACC TTCCGATACG GCTACCTTGT	240
TACGACTTCA CCCCAATCAT TTGTCCCACC TTCGACGGCT AGCTCCTAAA AGGTTACTCC	300
ACCGGCTTCG GGTGTTACAA AC	322

(2) INFORMATION FOR SEQ ID NO: 4396:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4396:

TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC	60
AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC	120
GTTTGTAGACA TAAAAAAGA nACCTCACGG TCCAAACTTG CCTGGCAACG TTCTACTCTA	180
GCGGAAnTGA ATTGGCTACC ATCGnCGCTA AAGACCTTTC TTGACTTGTTG ACAATCGCTT	240
GCTTCTTTCC TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT	300
CTT	303

(2) INFORMATION FOR SEQ ID NO: 4397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4397:

TAAGAATATA AATGATTTTG AAAGCATTTG AAGCTACAA CATTCTATA AAATTTTCA	60
ATAACAATTG CGCCACTAAA ACTCAAAAT TCCACCACCA ACATCCAAAT TATCAACATC	120
GCAACATAAC CAAATGTTAT AATAAATCTA TTACACAAAG AGATAAATTA CTTATGCAAA	180
GGCGGAGGAA TCACATGTCT ATTACTGAAA AACAACGTCA GCAACAAGCT GAATTATA	240
AAAAATTATG GTCGATTGCG AATGATTTAA GAGGGACATG GATGCGAGTG AATTCCGTAA	300
TTACATTTTA GGCTTGATTT TCCTATCGCh TCCTTATCTG GAAAAAnCCG ACCAGGATnT	360
GCAGATGCCT GGCCAGG	377

(2) INFORMATION FOR SEQ ID NO: 4398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4398:

TGCAATAACA GTATCTATGC CTAATTGTTT TGCAATGGCT TGAGCAGTGT TTTTATTATC	60
GCCAGTTAAC ATGGGCAACT TCAATGCCCA TATCATGGCA ATTGTTTAT AGCATCTTTG	120
GGCATGATnT TTGACAGTAT CTGCCACTGC GATGATACCA GTTAATGAAT AATTAACAGC	180

AATGAGCATA nCAGTTTTAC CATCTCGTTC ATATGTGTT AAATCATCAG AAATATGCTT	240
AAGCAACTAA TATCATTGTC AACCATTAAT TTACCGTTAC CAACCAATAT ATGGTGATGA	300
TCnATCCTTC CTC	313

(2) INFORMATION FOR SEQ ID NO: 4399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4399:

TGGCTATGAT CATCCAAAAT ATGGTGAATC AATTGCTGCA GCCATTATAC TTGCGAAGA	60
TGAACCTCAT TACGCTGAAA TTTTAAATCA ACATATGCGA AGTCGTTTAG CAGGTTATAA	120
AGTCCCAAGA ATGTATGTAC CAGTGACACA TATGCCGTTA AACAGTACGC AGAAACCAGA	180
TAAACTTGCG ATTCGACAAA TGATGAATGA CAAAGTCTCG CAAACACTTT AAAGGTGATA	240
AAAATTTTTG ACATTTAGTG TAAGCGTTTA CAAATAAAGC GTGTTGTTTT TGAATTAAAT	300
GCATTTTACA TTAGTATTCA TATTATnTTT AGGAGGAATT TATATGACAT TTGAAAAAGA	360
ACGGGCTTAA AACATTATTC CTGAGATGTA CTAGTATGCT	400

(2) INFORMATION FOR SEQ ID NO: 4400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4400:

CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT TTCGTCAGAT TCAAACGTTT	60
TCACTTCGCC AAGCCATTTT TCTTTGTGTT TACTTTTTAT TTTGACGTTT TAGACATAAA	120
AAAAGAGACC TCgtCTCAAC TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTGGC	180
TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTTCCT	240
TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC	300
ArATTCAAAC GtTTTCAcTT CGGCCAAGGC ATTTTCTTT GTGGTTACTT TTTAATTGG	360
ACGGTTTTAG GCATAAAAAA AAAGGGGACC CTGCGGGCTC nAAAGGGG	409

(2) INFORMATION FOR SEQ ID NO: 4401:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4401:

TCATGTAGAC TTTCAAGAAT CGACACATGA AAATTCAAAA CATCATGCTG ATGTTGTTGA	60
ATATGAAGAA GATACAAACC CAGGTGGTGG TCAGGTTACT ACTGAGTCTA ACCTAGTTGA	120
ATTTGACGAA GATTCTACAA AAGGTATTGT AACTGGTGCT GTTAGCGATC ATACAACAAT	180
TGAAGATACG AAAGAATATA CGACTGACAT mATCTGATT GAACTAGTAG ATGAACTACC	240
TGGAAGAACA TGGTCCAAGC GCAAGGnCCA ATCCGAGGAA ATTGACTGGA AAACAATCCA	300
TCCATATTTTC C	311

(2) INFORMATION FOR SEQ ID NO: 4402:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4402:

TTAACGGATT ATTTGGCAAT TCGGTTAGTT GTCGAACAAT TGCTAGTTGG GATGAGTTT	60
AAGTCAGTCG CTAAAGATTG TGAAAGTAGA TCGGAAAATT GGTTTAAGCA AACTGTTGCA	120
TCATGGTGTT ACTACAGTGA TATGCCTAGC GATGTATTAC TACAACATGG ACGTCAATGT	180
AAATTnCAAA CGTTTATTCA TTTTGGCAGC AACTATGGAA TAAAAATGTA TTTAAAAATT	240
TATGGCTAAT TGCCTGGGGA AATGACATAC GAATCTCAGG TTAAACAGA AAATTAAAGC	300
AGGTCCATGT nAAGTGTGGG CGGGnCGCAT	330

(2) INFORMATION FOR SEQ ID NO: 4403:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4403:

TGnTCACACA TAATTTGCGG CCATATGTTG TTGGCACTGG CCGTTTGTAT TATCTGGCAC	60
TTTGGGCCCA TATGTTGnCA AAATACGGC CAATTGCTTC TTTATAAGTT GTTATTTTTT	120

TACTTTTTCC ATCGATAAGC CATACCTCTG GATGATACAT ATGATGCCCC ATCGCAGACC	180
AATAGCGAAA TTCACCCGTT AAAGTTTCGA GCTCTGATAA TTGTATAGAC CATTGATGAT	240
TTTGAGGTGG TACTTGATAT AAATTTTCTT CTCTAAATA TTCATTTAAA ATGGTTCTGA	300
TAGCCGCATA CGCTGCCATG TTGTATTAAT CnTTAATTG	340

(2) INFORMATION FOR SEQ ID NO: 4404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4404:

TTAACATATA TTTTGGGACC TTAGCTGGTG GTCTGGGCTG TTTCCCTnnA CGAACACGGA	60
CCTTATCACC CATGTTCTGA CTCCCAAGTT AAATTAATTG GCATTCGGAG TTTGTCTGAA	120
TTCGGTAACC CGAGAGGGGC CCCTCGTGCC AAACAGTGCT CTACCTCCAA TAATCATCAC	180
TTGAGGCTAG CCCTGAAAGC TATTTCTGGGA GAGAACCAGC TGATTTCAG GTTCGATTGG	240
AATTTCTCCG CTACCCTCAG TTCATCCGCT CACTTTTCCA ACGTnAATCG GTTCGGTGCC	300
TGCCATT	307

(2) INFORMATION FOR SEQ ID NO: 4405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4405:

TTTTTTTAAAG TCTGATGTGA AAGCCACGG CTCAACCGTG ATGGGTCATT GGAAACTGGA	60
AnACTTGAGT GCAGAAGAGG AAAGTGGAAT TCCATGTGTA GCGGTGAAAT GCGCAGAGAT	120
ATGGAGGAAC ACCAGTGGGC GAAGGCGACT TTCTGGTCTG TAACTGACGCTGATGTGCGA	180
AACGTGnGGG ATCAAACAGG ATTAGATACC CTGGTAGTCC ACGCCGTAAA CGATGAGTGC	240
TAAGTGTTAG GGGGTTTCCG CCCCTTGAGT GCTGnCAGCT AAACGCATTA AGCACTCCGC	300
CTGGGGGAGT GACGGACCGC AAG	323

(2) INFORMATION FOR SEQ ID NO: 4406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4406:

AATTATGGGA TGCAATGGGA TACGAACGTG TTAAAACACG TATGGAAGAC GAACTTGGAG	60
ACTTACCACA ATGGATTAGT GATTTAGATG GTGGCTTTTA TAAACAAGAT GAGACCATTG	120
AATATGCAAC ACCTATTTCT CACTTCGTAA AAGATGAACT TTGGGATAAA GGTGATGCCA	180
AACTTTCCGT AACTCATGAT GATCACTGT TACTGAAATT ACAAAGTAAA AATAATGTCA	240
TTACCGATGA ATTCAACGGT GCGTTAGTTG ATGCGATTGA TTTACTGGGA AATGACCCTT	300
ACnCnAGnAT GGGTA	315

(2) INFORMATION FOR SEQ ID NO: 4407:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4407:

CACCACCTCC CTACCTACTC GCCCCCATC ATAAATAGG TGGACGAA TATCAACCTG	60
TTATCCATCG CCTACCCTGT CGCCTCAGCT TAGGACCCGA CTAACCCAGA GCGGACGAGC	120
CTTCCTCTGG AAACCTTAnT CAATCGGTGG ACGGGATTCT CACCCGTCTT TCGCTACTCA	180
CACCGGCATT CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT	240
AGAACGCTCT CCTACCATTG TCAAAGGAA TCnCACAGCT TCGGTAATAT GTTTAGCCCC	300
GGTACATTTT CGGCGCATGT CACTCGACTA nTG	333

(2) INFORMATION FOR SEQ ID NO: 4408:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4408:

ATTTAATGAA GTGCTTGTTA ATGAACCAAG CGCTAAAGAT ACTGTTGAAA TTTTAAAAGG	60
TATTCGCGAA AAATTCGAAG AACACCATCA AGTAAATTA CCAGATGACG TATTAAAAGC	120
ATGTGTTGAC TTATCAATTC AATATATTCC ACAACGATTA TTACCAGATA AAGCAATCGA	180

TGTGTTAGAT ATTACAGCAG CACATTTATC TGCGCCAAAGT CCCAGCTGTC GATAAAGGTT	240
GAAACTGAAA AACGGATTTT TGGATTnGA AAATGATAAA CGTAAAGG TAAGTGCTTG	300
AAGGGATTTT AAAAAAGCTG ACGGACCATT CCAAATTGG AATCCAAATC nnTTACCAGG	360
TTAAATTTGG GAAAATGGTT AATTGGTGGG ACC	393

(2) INFORMATION FOR SEQ ID NO: 4409:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4409:

GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC	60
TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA	120
GCCATTTTTT TTTGTGTTTA CTTTTTATTT TGACGTTTTA GGCATAAAAA AAAGAGACCT	180
TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTTCCTG GCAACGTTCT ACTCTAGCGG	240
AAGTnAATTG GGCTACCATC GTCCTTAAAG ACCTTCTTGT ACTTGTGGAC AATCGCTTGG	300
CnTCTnTCCT CTCCTTCGG	319

(2) INFORMATION FOR SEQ ID NO: 4410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4410:

AATTAAACAT TTCATTTTAA TCAATGAGAC TAAATACGC CTAACCTCGT TAACTTTTAA	60
AATGTATTAA AATTCTAAAG TTTCTTTTGC TTTTTCnATG ATGCTTTTTT TGTTTGGTAA	120
CCAAACATTT TCAGCTTGAG TGAATGGATA AATTGTATCT GCCTGCCTGA ACTCTTCCAA	180
TAGGTGCTTC TAATGAAAGG ATTGCACGTC ACTTAATTCA GCTAACAAC TCTGCACCAA	240
CACCAGCTTG CnGTTGTGCT TCTTGACTAC AACTGACGA CCAGTTTTTC AACTGAGCAC	300
AATTGTGCAC ATCGATTGGT GACAG	325

(2) INFORMATION FOR SEQ ID NO: 4411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4411:

GAGTTGGACA ATGCCGAAGC GTGAGCAAAG TTTTACCAT GCATGGTTGC ATTTAGCGCA	60
ACATGACCAT AGTTTTACTA AAGCACAGCG CCAAGTGATT AAAGGCTTAC CCAATGATCC	120
TGAAATGACG ATAGAGTCAG TATTAActCA TTTTCAATA GATCAGGAAG ACTAnCAAGC	180
TTATGTTGAA GGACATCTTT TGGCGTTACC GGGTTnGGCA nGTATGTTGT ATTACCGTTC	240
ACCACAGCAT CACTTTGAAC CACCTTTGTT AACGGGTAA TTGGCCATTC GGGTAAGTTG	300
TCCGACCATT GCCAAGTGGG TGATGAGTn AGGCCAGTCC GCAAAEATT GGGAAAGTAG	360
TCCGGAAAAT GGGTTAAGCC AACCTGTTGC CATCCAGGGG	400

(2) INFORMATION FOR SEQ ID NO: 4412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4412:

GATATATGGC AGCTCAAAGG AATGGGTTTC AGTTGAAGTG AAATTATCAC AGTCACTAGA	60
CCCGAGCACA TTATTTTCATC TCACTGACAA TGAGGCAGGA GATCGCTTTT ATATGCGTTT	120
GAATGATAAT CGAACGTCAT ATTTTGGCTA CAAAGCAATT CAATTATTCA AAAATAATTC	180
TAAAAATAAA CAATCTATTT TAAAAGACTG GGGAAAATTA AACATAACCA TCACCATTTA	240
TACCATCCGC nATTCTGGGA ACCATCATCC TTCGAGTTGT TGGAGGGTTC CATTTCCAAG	300
CCATAAATCA GATGATGAAT GEGnGAGTT TGGCCTAAAn CATTTGGAAT ACCCGGAGTT	360
TTAATTCCA	369

(2) INFORMATION FOR SEQ ID NO: 4413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4413:

TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT	60
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TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGTCTTTTC TCGTTTCGTC	120
AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC	180
GTTTGTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCnACTCTA	240
GCGGAAGTAA GTGGGCTACC ATCGTCGCTA AAGACCTTTC TTGGACTTGT GGACAAnCGC	300
TTGCGTCCTT nCCTC	315

(2) INFORMATION FOR SEQ ID NO: 4414:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4414:

GACCATCTCC TAAGGCTAAA TACTCTCTAG TGACCGATAG TGAACAGTA CCGTGAGGAA	60
AGGTGAAAAG CACCCCGGAA GGAGGTGAAA TAGAACCTGC AAACCGTGTG CTTACAAGTA	120
GTCAGAGCCC GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT	180
TTGATGCAAG GTTAAGCAGT AAATGTGGAG CCGTAGCAGA ACAGGGTCTG GAATAGGGCG	240
TTTAGTATTT GGTCGTAnCC GnAAACCAGG TGATCTACCC TTGGTCCAGT TGAAGTTCAG	300
GTTnACACT	309

(2) INFORMATION FOR SEQ ID NO: 4415:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4415:

TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA	60
TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT	120
CTCAAATGCG GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAAnTA	180
AGTTCGGACT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG	240
TGACCTCCTT GGCTATAGTC ACCAGnACAT ATGAATGTGA AATTTATACA TTCAAAACTn	300

(2) INFORMATION FOR SEQ ID NO: 4416:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4416:

AGAAAAATAA GCGAACTGnA ATAAATAAAG ATTCAATTAA CGCATCAGTA TTAGGATTCA	60
CTCTAAAACG ATTAATAGTT TTATAAGAAG GTGTTTGATC TTGAGCTAAC CACATCATTC	120
GAATACTGTC ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT TGAGTATATG	180
CATATAAGAT GATTTTTTAAC ATCATCTTTG GATGATAGGA TGTTGCGCCA CGATGATGTC	240
TGAATTCATC GAATTTGCTA TCAGGTATCG TTTCAACAATTCATT	286

(2) INFORMATION FOR SEQ ID NO: 4417:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4417:

TTTGATAAAA ATGGGCCATC GTCACGAGCT TCAACAATTC GTTTCGCAAC GTTTTCGCCA	60
AGCCCAGCCT GATATATTAC ATGAGGAGCG GTGCAAATGT TGTTAGAAAT TAAAGATTTA	120
GTGTATAAAG CGAGCGATAG AATCATACTA GATCATATCA GTCTAAAAGT AGATAAAGGC	180
GAGAGTATTG CCATTATAGG TCCATCAGGT AGTGGTAAAA GTACATTTCA AAAGCAAATA	240
TGTAATTTGT TTAGTCCAAC TAGTGAGAGAA CTTTATTTTA AAGGTAAACC CTATAATGAT	300
TATGACCCGG AAGAATTGCG TCAACGAATC CAGTTATTTG GATGCAGCCA AAGTGGACTT	360
GTTTGGTGGA ACGnATTGGA nGATAACCAT GGATAATTCC	400

(2) INFORMATION FOR SEQ ID NO: 4418:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4418:

GTATTTACAA TCAAATAAG CAAAAGTATT CAGATGCCTC AGATAAAGCT TGGGCGCATT	60
CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA CGCATATAAA AGTGCAAAGG	120
GTTGGCTAAT AGATATGGCT AATAAATCGC GCTCGAATG GGATAATATT TCTAGTACAG	180

CATGGTCGAA TGCAAAATCC GTTTGGnAAA GGAncATCGA AATGGTTTAG TAACTCATAC 240
 AAATCTTTAA AAGGTTGGAC TGGGGATATG TATTCAAGAG CCCACG 286

(2) INFORMATION FOR SEQ ID NO: 4419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4419:

CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT AGAACGCTT 60
 CCTACCATTG TCCAAAGGnA TGCnCACAGC TTCGGTAATA TGTTTAGCCC CGGTACATTT 120
 TCGGCGCATG TCACTCGACT AGTGAGCTAT TACGCACTCT TTAAATGATG GCTGCTTCTA 180
 AGCCAACATC CTAGTTGTCT GGGCAACGCC ACATCCTTnT CCACTTAACA TATATTTTGG 240
 GACCTTAGCT GGGTGGTCTG GGCTGTTTCC CTTTCGAACA CGGACCTTGA TCACCCCATG 300

(2) INFORMATION FOR SEQ ID NO: 4420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4420:

AGAAAATAGG TGTCCCGTAC CGGCAAACCG CACACAGGTA AnTCAAnATG AGAATTCTAA 60
 GGTGAGCGGA GCGAACTCnC GTTAAGGAAC TCGGCAAAT GACCCCGTAA CTTCGGGAGA 120
 AGGGGTGCTC TTTAGGTTAA CGCCCAGAAG AGCGCAGTG AATAGGCCCA AGCGACTGTT 180
 TATCAAAAAC ACAGGTCTCT GCTAAACCGT AAGTGATGTA TAGGGGCTGA CGCCTGCCCCG 240
 GTGCTGGAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAAcT ACGAATCGAA GCCCCAGTAA 300
 ACGGcGGCCG TAACTATAAC GGTCTAGACG ATCTGC 336

(2) INFORMATION FOR SEQ ID NO: 4421:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4421:

GGnCACCCCTC GTGCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG GCTAGCCCTA	60
AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTGCATT GGAATTTCTC CGCTACCCTC	120
AGTTCATCCG CTCACCTTTT AACGTAATCG GTTCGGTCCT CCATTCACTG TTACCTGAAC	180
TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT AAACGCCCTA	240
TTCAGACTCG CTTTCGCTAC GGCTCCACAT TTAAGTCTTA ACCTTGCATC AAATCGT	297

(2) INFORMATION FOR SEQ ID NO: 4422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4422:

GTACATCGTC TAATAATAAG TTGACGATAT CTTGCAATGC ATCTTTATCT AAATGTAAGA	60
ATTCAACGAT GCCGTTGAAG CGGTTAAGGA ATTCAGGGCG GAAGAATTTT TTCATTTTCGT	120
GCATAATATC TTTTCTTCA GCGTCATTGC CATTGCCAAA GCCAGCATTT GATGTACAAA	180
TAATAATTGT ATTTTAAAG TTGATGACAT TACCTTGACC ATCAGTCAAA TTACCATCAT	240
CCATTACTTG TAATAACAAT GTTAAAATTG TGGATTGCTT TTCGATTCA CAATGAATG	300
ACTGAGAnGG GATACGGCGA CTTTTCAGTA AACGGATTGA ATGGCATCAT AnCCACATAC	360
CAGCGTGGAC CATCATTTTG GAACAGCGTG GGCACATATC	400

(2) INFORMATION FOR SEQ ID NO: 4423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4423:

AAGTTGAGTC GCATAGCTAG TATGAAACGT GGTGTGCGCA TGGGAACAT CAAGCTTTGA	60
AGATGTGGTA CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT	120
CCATTAAATG AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT	180
AAAATTGCCT ATAAATTTTT AGCACATAAA ATAAGAnGn CCAACCATTT TTAGACTATA	240
ACAACGGTTG GCTCTTTAAT TGTAAAAAGA AACCATACG CTATGGTAGT T	291

(2) INFORMATION FOR SEQ ID NO: 4424:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4424:

AACTGCCACC ACCTGGGGnC GTTTCAGAA CCTCTATGCA TTTCAATCAC AGnCAAATGT	60
GCGGTTGACG TTCAATGACT ACCTGCAATT CATCGGTCAG CTCACACCCT TTACCTGnCT	120
AAAGTACCAG TAGACAATGT AGGTATTGGA CTTGCATGAG CATTTTTATn AGTAATGGG	180
CTTTAGATAT TTTATTAATA CCGGCCAATC ATGCTATTCA AACCGCCAAT AGCTTTATTA	240
GCAACATTTT TACCTAAATC AGCCGCAGCT CTTCCCATGT CTTTACCAAT ATCTCTAATC	300
CAATCATATG TTTTGCATA GCCATTTTCT AAAACCATTA AATACTGATT TAGCGTTAGA	360
CCATGCCGAA CTTGAAATTG CATCAAAACG ATCGTGGGCT	400

(2) INFORMATION FOR SEQ ID NO: 4425:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4425:

CTTTGACAAT TTGTATACCG TACTATCTTG CGCTTATTGA AGTAATGAAT GAAACACCTA	60
AGATGATAAAA AGCAACAGGT GGTTTTGC GA AAAGTGAAGT ATGGCGTCAA ATGATGTCAG	120
ATATATTTGA CACAGAGTTA GTGGTTCCTG AAAGTTATGA AAGTTCATGC TTAGGTGCCT	180
GCGTGCTCGG ACTTAAAGCT GTAGGTGACA TTGAAGATTT TTCAATCGTT TCATCGATGG	240
TCGGTGCCAC AAACAATCAT ACGCCGATTG AAGAAAATGC ACTGTTACCA AGAnTCGAAT	300
CCATTnTTAT CATTAGCGT CTTAnCAGAG ATATGACAAT	340

(2) INFORMATION FOR SEQ ID NO: 4426:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4426:

CTGAAGATGA TAAAGATGCA GATGGTGGCG AGTTGCACGT AACAATTACG GATCATGATG	60
ATTTACACT TGATAACGGA TACTTCGAnG AATTATCATC AGACAGCGAT TCAGACTCAG	120
ATAGTGACTC AGACAGCGAC TCAGACTCAG ACAGCGACTC AGACTCAGAC AGTGATTTCAG	180
ATTCAGACAG CGACTCAGAT TCAGATAGCG ACTCAGATTTC GGACAGCGAT TCAGACTCAG	240
ATAGCGACTC AGATTTCAGAT AGCGATTTCAG ACTCAGACAG CGACTCAGAT TC	292

(2) INFORMATION FOR SEQ ID NO: 4427:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4427:

AACAGTGCTC TACCTCCAAT AATCATCACT TGAGGCTAGC CCTAAAGCTA TTTCGGAGAG	60
AACCAGCTAT TTCCAGGTTC GATGGAATT TCTCCGCTAC CCTCAGTTCA TCCGCTCACT	120
TTTCAACGTA ATCGGTTTCGG TCCTCCATTC AGTGTTACCT GAACTTCAAC CTGACCAGGG	180
TAGATCACCT GGTTTCGGGT CTACGACAAA TACTAAACGG CCCTATTCAG ACTCGGCTTT	240
CGCTACGGTT CCCACATTTA CTGGCTAAAC CTTGCATCAA AATCGGTAACTCGnCGGGTC	300
ATTCTAn	307

(2) INFORMATION FOR SEQ ID NO: 4428:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4428:

GACCATACAT CGTCATCGTT TGCACCGTCA AATACTGGTG ATGCAACGTG AATACCAAGA	60
TTTTTAGCAG CCATACCTAA GTGTAGCTCT AATACTTGTC CGATGTTTCAT ACGAGATGGT	120
ACACCAAGAG GATTTAACAT GGATATCGAT CGGGACGTCC ATCTGGTGAA GTGAAGGCAT	180
ATCTTCTTCA GGGAACAATC TTGAGGAAAT GGACACCTTT GTTGACCATG TCGGACCACA	240
CATGCTTATG CACCAACATG GAATTTTACG TTTTGGAAAn GATGATTATT ACACGTnACT	300
AATTGGTTTA CACCAGGTGG AnAATGTTAT CGTCGGCCTT GCTTCACGAT TGGA	354

(2) INFORMATION FOR SEQ ID NO: 4429:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4429:

GTGnACTATC nGCTTGTCTA TGATAATATT ATTCTTTGTA CTTGTTTAAA AGATATTAGA	60
CTAAAACTAA AAACAGCAGT AAGATGATTT ATGATTAAAA CTATCTTACT GCTGTTCACT	120
TTTTATAATA CTTCTGAATG TCTCACTTAT ACTTCTAGTC ACAGATTAA ATAATCAAAA	180
GTGCACATTA TTAAAATATC AATTTACACAC TCAATGCGGC TCATCGCATT CATTCTTGT	240
CTAGCAACGT TCTACTCTAG CGGAACGTAA GTAGCTACCA TCTCGCTAAG GAACTTTCTT	300
GACCTGGTGA CAACCGCTGC GnCTnTCTCT CTTGGGCTCT CGCTTACTCC ATTTAGCTCC	360
ACTAAACTCG TCGGGCCCTT CCCGTTCGGC AGATCCAACG	400

(2) INFORMATION FOR SEQ ID NO: 4430:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4430:

ACTGCCATCC TTCAATCGGn ACGACATTTT TCTTGTTCCC ACATAGTGAG CCCAACCGCC	60
ACCATTACACA CCTTGACAGC CACATAACAT AACTAAGTTT AAGATnGGGG GATAAATCGT	120
ATCTGAGTTA AACCAATGGT TATACCCGC ACCCATGATA ATCATTGAAC GCCCTTCAGT	180
ATCGATAGCG TTTTGCGCAA ATTCTTTTCGC TACTTGAATG ACAACACTTT GTTTTACGCC	240
TGAAATGGCT TCTTGCCAAG CAGGTGTATA TTTTGATTCT GCATCGTCGT AA	292

(2) INFORMATION FOR SEQ ID NO: 4431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4431:

TGAGCCGnAC ATCGAGGTGC CAAACCTCCC CGTTCGATGT GACTCTTGG GGGAGATAAG	60
CCTGTTATCC CCGGGGTAGC TTTTATCCGT TGAGCGATGG CCCTTCCATG CGGAACCACC	120

GGATCACTAA GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCATC AAGCTCCCTT	180
ATGCCTTTAC ACTCTATGAA TGATTTCCAA CCATTCTGAG GGAAC TTGA GCGCCTCCGT	240
TACCTTTTAG GAGGCGACCG CCCAGTCAAA CTGCCCCGCT GACA	284

(2) INFORMATION FOR SEQ ID NO: 4432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4432:

TATCATTGTG GTACGATAAG GCATATGTTG TACCTATGnA TGGTGGAAGA GCCTTCAGTT	60
GTCGCTGCAG CTAGTTATGG TGCAAAGCTA GTGAATCAGA CTGGCGGATT TAAAACGGTA	120
TCTTCTGAAC GTATTATGAT AGGTCAAATC GTCTTTGATG GCGTTGACGn TACTGGAAAA	180
TTATCAGCAG ACATTAAAGC TTTAGAAAAG CAAATTCATA AAATTGCGGn TGAGGCATAT	240
CCTTCTATTA AGCGCGTGTG GTGGTTACCA CGTATAGCGA TTGATACATT CCTGGCCACC	300
AGTTCTATCT TT	312

(2) INFORMATION FOR SEQ ID NO: 4433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4433:

CGGTACTCGT TAAGGCTGAG CTGTGATGGG GAGAAGACAT TGAGTCTTCG AGTCGTTGAT	60
TTCACACTGC CGAGAAAAGC CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC	120
AGGTAGTCAA GATGAGAATT CTAAGGTGAG CGAGCGAACT CTCGTTAAnG AACTCGGCAA	180
AATGACCCCG TAACTTCGGG AnAAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC	240
AGTGAATAAG CCCAAGCGAC TGTTTTATCC AAAACACAGG TCTCTGCT	288

(2) INFORMATION FOR SEQ ID NO: 4434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4434:

GGACCGAACC GACTTACGTT GAAAAGTGAG CGGATGAACT GAGGGTAGCG GAGAAATTCC	60
AATCGAACCT GGAGATAGCT GGTTCCTCTCn nAAATAGCTT TAGGGCTAGC CTCAAGTGAT	120
GATTATTGGA GGTAGAGCAC TGTTTGGACG AGGGGCCCT CTCGGGTAC CAATTCAGA	180
CAAACCTCCGA ATGCCAATTA AATTAACTT GGGAATTCAG AACATGGGTG ATnAAGTCCG	240
TGTTTCGAAA GGAAACAGCC CAGACCACCA GCCAAGTCCCAAAATATATG TTTAATGGGA	300
AAAGGTGTGG CCTTTGCCCA GGACAACCAA GAAGTT	336

(2) INFORMATION FOR SEQ ID NO: 4435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4435:

ATTGACGCCG CATTTTTACG GAATGGGAAT AAAGCGACAC AAACCGTCAC GTCnGTGTTG	60
GTGTCATGAC AAGGTAATGC GAGTGATCTG ATGTATGGCT TATCATGGCA ATCTGTTATG	120
GnCTGACTGA TCGGACGATG TATCATTCGC CAATTCGTTT ACTTGTCGTT ATTCAGGCAC	180
CCGACTATGT TGTAGGCAAG ACTACTCGCG AATAATGAGC ATTTGCTAG GAnGTGTCTA	240
AATCATTGGC TGC GTTTTAA TGAGCGTAAT GAGGAAGGGG CGTTTAAAAA GTTGGATTTA	300
ACGA	304

(2) INFORMATION FOR SEQ ID NO: 4436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4436:

AATATACTCC GGTAATAAC CGAAGAGTTT TGAATCATTG TAAAAATGG AATTAnAGTT	60
CTAGTATCTG TTGGGTTTTG AAATAGGTCA TAGGATAAAA CAAATnGAGA ATTTGTCGCT	120
ATTTGTAAAT TGTATCCTGG CTTAAGTTGG CCATTTTCA TATGGTCTTC CTTATTCTC	180
ATAAAAGTTG CATCATGGAT CAGTTTTAGA AAAGCTATTT CTATCTTTAA GAATCGATTT	240
TTGTTCTTCA TATTTATTTT TTCTTTCGGA ATAATCATCA AATTTATnTT TGGAACCTCT	300

(2) INFORMATION FOR SEQ ID NO: 4437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4437:

ATCGTTTAAA TCAGTTAGTA AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAAATA	60
TTATAGAAAA CATCAAAGGA TGTTAAGAAA TACAATTTAT TACCCAGCAT TTAATAATGG	120
TGCTATAGAA GGAATTAATA ATAAGATAAA ATTAATCAAG TGAATTTCTT TTGGTTACAG	180
AAATTTCAAC AACTTTAAAG CACGTATAAT GATGATTTTC AGCTTGTACA AGGGGGAnAA	240
AAGGAnGnCA ACCAAGCCCA ATAATGGACT GGCCGCCTAA TATTAAAAAC TCTAAAGGTT	300
GTATTTTAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA CCCGTTAAC	359

(2) INFORMATION FOR SEQ ID NO: 4438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4438:

ACTTACAGTT ATTTTAACTT GGnCAGAATC CATATCCAT AAGTTCGAAA TGTTGTAAAA	60
CATAAACCTT GnAAACGGCA ACATTTTGG GTCCTTCTCC ATCATTTTAT TTAAAAGCGC	120
ATTATGATCA ATATCATGCC CAATTAAGTT TCCAGCAATT TCCATAGTAT GTTCTGAGGT	180
ATTGTTAAAA AGGAATCGCC CAGTATCACC GACGATACCA AGATATAAAA CGCTCGCGA	240
ATCTTTATTA ACAATTGCTT CATCATTAAT ATGTGAGATT AAATCG	286

(2) INFORMATION FOR SEQ ID NO: 4439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4439:

TCGCTTGACT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAnCTCT ACTAAACTCG	60
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TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT	120
TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA	180
TGCGGCTCAT CGCATCCATT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG	240
GCTACCATCG ACGCTAAGAA CCTtTCTTGA CTTGTGACAA aTCGCTTGCT TCTTTCCTCn	300
TCTTCGGTCT CGCTTACTCA TTTAGCTCTA CTAACTCGT TGCGCTCTTT TCTCGTTTCG	360
TCAGATTCAA CAGTTTTTCAT TCGCCAAGCC ATTT	394

(2) INFORMATION FOR SEQ ID NO: 4440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4440:

TAATAGGTTC GAGGTGGAAG CATGGTGACA TTGGCAGCTG ACGAATACTA ATCGATCGAA	60
GACTTAATCA AAATAAATGT TTTGCGACAA TGCAACTTTT ACTTACTATC TAGTTTGAA	120
TGTATAAATT ACATTCATAT GTCTGGTGAC TATAGCAAGG AGGTCACACC TGTTCCCATG	180
CCGAACACAG AAGTTAAGCT CCTTAGCGTC GATGGTAGTC GAACTTACGT TCCGCTAGAG	240
TAGAACGTTG CCAGGCAAAA AATGGATGCG ATGACCGCAT TGAGACCGCA GCnTn	295

(2) INFORMATION FOR SEQ ID NO: 4441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4441:

TTTCATAAAA AGATTTCAA CGCGTTCATC AAnCCTCGTC GCAGGTCTTT CGAACACTAG	60
CGATTATTTT tTATGAATTC AAGCTTATTT AAAACTCTTT ATTCaCTCGG TTTTGCTTGG	120
TAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA CAATTTCTTT TTAGTCAAGC	180
GCTCGCATAC TGCTTTATTT TCATAAGCAA ATCACTTTA ACCAAAAAAT ATTTGAATGT	240
TAAATAAACA TTCAAACTG AATACAATAT GTCACGTTAT TCCgCATCTT CTGAAGAAGA	300
TGTTCCGAAT ATATCCTTAG AAAGGAGGTG ATCCnGCCn ACCTT	345

(2) INFORMATION FOR SEQ ID NO: 4442:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4442:

AATCATTGTC AAAACTACGT TCTGGTAAAC AAGGACAACC CGTTTGAACC ATGGCCCCAC	60
ACCATTTGAT AGGCAGnCAT GTGCGCAATG GACATCCACA TAGTTGCGTA ATGTTTCATA	120
CGTCATTGCT CAAATCATTC ATGACTAGCG CAACATGATT ACCTTGTCGT GnGCACCTTC	180
ATTAAAGnAA CTTATGATAG ATTTATTTCC CGGGACATTA AGCATTCGCA TCGTTAACAT	240
GCGTATTGCA CCCAATTTAG AAGTTCCTCC GTGCCGTTTG GTATATCACA AATTTGTAGT	300
GTATCTTGGA TGC	313

(2) INFORMATION FOR SEQ ID NO: 4443:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4443:

AGCATGGTGT TTCTCAGATT GTCGGATGTA TAAATGTGTA TGTTATGTTT TAATTTTTTCC	60
CAGTCTTTAA AAATAGATTG TTTATTTTGA GAATTATTTT TGAATAATTG AATTGCTTTG	120
TAGCCAAAAT ATGACGTTTC ATTATCATTC AAACGCATAT AAAGCGTATC TnCTGCCTCA	180
TTGTCAAGTGA GATGAAATAA TGTGCTCGGG GTCTAGTGAC TGTGGATAAT TTCACCTCAA	240
CTGAAACCCC ATTCCCTTTG AGCTGCCCCAT ATATCTCTTT GGACAATATC GGTCCTCTA	300
ATACGGnCCG TAGnCCATTC CATTTCAATT CTTTTT	336

(2) INFORMATION FOR SEQ ID NO: 4444:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4444:

CAGACTGGGA TATTTATAAA ACGTTGGCAA AAGCATTTTC AGAAATGGCA AAAGACTATT	60
TACCTGGAAC GTTTAAAGAT GTTGTGACAA CTCCACTTAG TCATGATACA AAGCAAGAAA	120

TTTCAACACC ATACGGCGTA GTGAAAGATT GGTCGAAGGG TGAAATTGAA GCGGTACCTG	180
GACGTACAAT GCCTAACTTT GCAATTGTAG AACGCGACTA CACTAAAATT TACGACAAAT	240
ATGTCACGCT TGGGCCTGTA CTTGAAAAAA GGGGAAATTT GGAGCACCTG GGGGTAAGTT	300
TCCGTGTCCA GTTGAACCAT TATGGAGGAn TTnAAAAAGT ATGTTAAGGG ACCTGGGAGT	360
TGAATACCCA ATGGATnGAT TCCCGTGAAG AGCCGAATCC	400

(2) INFORMATION FOR SEQ ID NO: 4445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4445:

TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA GCTCGCGTAC	60
CGCTTGTAAT GGGCGAACAG CnATCGCCTT GGGACCGACT ACAGCCCCAGGATGCGATGA	120
GCCGACATCG AGGTGCCAAA CCTCCCCGTC GATGTGAACT CTTGGGGGAG ATAAGCCTGT	180
TATCCCCGGG GTAGCTTTTA TCCGTTGAGC GATGGCCCTT CCATGCGGAA CCACCGGGAT	240
CACTAAGTCC GTGCTTTCGA CCCTGACTAC GGA CTGTnA GGTCTGCGGC ATTCAAGCTT	300
CCCTTGATGG CCTTTGACAC TGCTTATGGA ATGnATTG	339

(2) INFORMATION FOR SEQ ID NO: 4446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4446:

CAATTTTAAG TGTTGAAAAT GTCAC TTTTA AACTTTCTAG TTTTATCTTT AATAAACATG	60
CCATnCGTAA TAAGTGGCGT TTTATTAAAA TCATCTATAA TAGCCATATA GTTTTGCTCA	120
CTACCATAAC CTGCATCAGC TACAAATATAC TCCGGTAAAT AACCGAAGGA TnTTTGGAAT	180
CATTGT TAAA AATGGAATTG AAAGTTCTAG TATCTGTTGG GTTTTGAAAT AGGTCATAGG	240
ATAAAACAGG GTGAGAATTT GTCGCTATTT GTAAATTGTA TCCTGGCTTA AGTTGGCCAT	300
TTTTnCATAG GTCTTCCT	318

(2) INFORMATION FOR SEQ ID NO: 4447:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4447:

TTTTGAAATT CTCTATGTTG GGGCCCGGAC TATAATTGAA AAATGCTTGT TACAAGTGCA	60
TTTTATTTCA GTCAACTACT AACAAATATAA CATTGTGGAG CCCAGAnCTT TGATTAATGT	120
ATATGAAAAT CAAAGTAATG CTTATGTATG ATTATTTCAA ATATTTTACA TACATGAACT	180
TTTCCAATGT ACGATACTAT TATTATAAAG CGCTCGCTAA GATTTTACGA TGATTAGAGG	240
GTAAAAAATG AACGATCAAT GGTnTAACCA TTTAATTGG	279

(2) INFORMATION FOR SEQ ID NO: 4448:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4448:

GACACCGGCA TTCTCACTTT CTAAGCGCTC CACATGTCCT TACGATCATG CTTCAACGCC	60
CTTAGAACGC TCTCCTACCA TGTCCAAAG GACAATCCAC AGCTTCGGTA ATATGTTTAG	120
CCCCGGTACA TTTTCGGCGC AGTGTCCTC GACTAGTGAG CTATTACGCA CTCTTTAAAT	180
GATGGCTGCT TCTAAGCCAA CATCCTAGTT GTCTGGGGCA ACGnCACATC CTTTTCCTACT	240
TAACATATAT TTTGGGACCT TTAGCTGGTG GTCTnGGGCT GTTTTCTGA TTGAACACGG	300
GA	302

(2) INFORMATION FOR SEQ ID NO: 4449:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4449:

CGTTGGTATA TAGAGGGCAA CCGTCACCTG ATAAAATGTG GACACAGTTT TTACAAGAGG	60
TTAAGGAAAT GAGTTTGGAG GCATACGAGC ATCAAGAATA CCCATTGCGAA TGTTTAGTAA	120
ATGACTTAGA TCAATCACAT GATGCCTCAC GGAATCCATT ATTTGATGTC ATGTTAGTAC	180

TACAAAACAA TGAnACGAAA TCATGCTCAT TTTGGGCATA GTAAATTTAA CACACATTCA 240
 ACCCCAAATC AGTGACGGGC GGAAATTTGG ATTTnTCCTT TTCCATCATT GGAAGAAGGA 300
 TCGCGGATGA CCTAATAnCA ATCAATTAT CGGGGTATAA ATACCGGATT TTATAACCA 359

(2) INFORMATION FOR SEQ ID NO: 4450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4450:

GATGACAAAA TTTGCTTGAA AACCGAAATG GATGGTCATC ATTGACTGnA TCAAGGTACA 60
 TCATTCTTTG GTGCTTATGC ATTTAGACAT TATACAAAAA CAATACTTTT ATAGGGCAAC 120
 CTTATGGGGT TCTATCGGCT ATACATTACC TGCAACATTA GGTEACAAT TAGCAGACAA 180
 AGATCGTCGn TAACTTATTA TTAATTGGTG ATGGCTCATT GCCAACTAAC TGTTCAAGCT 240
 ATTTCAACTA TGGATTAGAC AGCATATTAA ACCGGTATTA TTTGTGGATT AATAATGACG 300
 GCTATACGGT AGAACGACTT ATTCCC 326

(2) INFORMATION FOR SEQ ID NO: 4451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

GAAAACATCA AAGGATGTTA AGAAATACAA TTTATTACCC AGCATTTAAT AATGGTGCTA 60
 TAGAAGGAAT TAATAATAAG ATAAAATTAA TCAAGTGAAT TTCTTTTGGT TACAGAAATT 120
 TCAACAACTT TAAAGCACGT ATAATGATGA TTTTCAGCTT GTACAAAGGA GAnAAAAAGA 180
 AGACAACCAA GCCCAATAAT GGA CTGGCCG CCTAATAATA AAAACTCTAA AAGTTGTATT 240
 TTAAAAATAG GTCTTTAAAT TATATACCCC CCCCATTTGG GTGGAGAACC GGTAACCAT 300
 GCCTAGGTGC CTAACCTCCn ATAATGGnAC CCCTCCTTAC CATTTGGGCC ATGGGGCCAA 360
 TAAAGCGGGG GGCAATTGGG G 381

(2) INFORMATION FOR SEQ ID NO: 4452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4452:

TTAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG TTATTAATCT TGTGAGTGTT	60
CTTTTGAACA CTAGCGATTA TTTCTTATGA ATTCAAGCTT ATTTAAAACCT CTTTATTCAC	120
TCGGTTTTTGC TTGGTAAAT CTATATTTTA CTTACTTATC TAGTTTTCAA TGTACAATTT	180
CTTTTtagTC AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAAATAT TTGAATGTTA	240
AATAAACATT CAAAACTGAA TACAATATGT CACATn	276

(2) INFORMATION FOR SEQ ID NO: 4453:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4453:

GGCGAAACCG CGTAGCGTTT TTAAAGTCTG ATGTGAAAGC CCACGGTCAA CCGGGAGGGT	60
CATTGGAAAC TGGAAACTT GAGTGCAGAA GAGGAAAGTG GAATTCCATG TGTAGCGGTG	120
AAATGCGCAG AGATATGGAG GAACACCACT GAGCGAAGCG ACTTTCTGGT CTGTAAGTGA	180
CGCTGATGTG CGAAACGTGG GGGATCAAAC AGGATTAGAT ACCCTGGTGA GTCCACGCCG	240
TAAACGATGA nTGCTAAATG TTAGGGGGTT TCCGCCCTT AAGGCTGCC AGCTAnACGC	300
ATTGAAGCAC TGCCGCCTGG GGAGTGACGA CCGCAAnTTG A	341

(2) INFORMATION FOR SEQ ID NO: 4454:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4454:

ACnCTCCCCA AAGTCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA GTGnCCAAGG	60
CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTTTAT AAGTCAAACG	120
CTCACATACG GCTTCGTTTT CATTATTTTA AATGCTCATT TACATAAGTA AACTCTGCTT	180
TAAATAATT TAACTCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT TTAAACGCGT	240

TATTAATCTT GTGAGTGTTT TTTGGAACAC TAGCGATTAT G 281

(2) INFORMATION FOR SEQ ID NO: 4455:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4455:

ATGTCTTCAC TTATACTTCT AGTCACAGAT TTAAATAATC AAAAGTGCAC ATTATTAAAA 60
TATCAATTTT ACACTCAATG CGGCTCATCG CATTCAATTTT TTGTCTAGCA ACGTTCTACT 120
CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGAACAATC 180
GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCAT TAGCTCTACT AAACCTCGTTG 240
CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCTnGT 279

(2) INFORMATION FOR SEQ ID NO: 4456:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4456:

ATTTTGACGT TTTAGGCATA AAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT 60
CCATTTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGT 120
AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTT CTCTCCTTCG GCTCTCGCTT 180
ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TnTCGTCAGA TTCAAACGTT 240
nTCACTTCGC CAAGCCATTT TTCTTGTGTT TACTT 275

(2) INFORMATION FOR SEQ ID NO: 4457:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4457:

ATCCGATTCA CAAAGCACAT CATCATATAC AAGTCAGTCA ACAAGCCAAA GTGAATCCAC 60

ATCGACATCA ACGTCACTAA GCGATTCAAC AAGTATATCT AAAAGTACGA GTCAATCAGG	120
TTCGGTAAGC ACATCAGCGT CATTAAGTGG TTCAGAGAGT GAATCTGATT CACAAAGTAT	180
CTCAACAAGT GCAAGTGAGT CAACATCAGA AAGTGGTCA ACATCACTCA GTGACTCAAC	240
AAGTACAAGT AACTCAGGAT CAGCAAGTAC GTCAACATCG CTCAGTAACT CAGCAAGCGC	300
AnTGGAAATCC GATTTGTCGT CAACATCTTT AAGTGGATTC AACATCTGCG TCnATGCCAA	360
AGnnGTGAAT CCGATTCAACA AAGCACATCA GCATCCTTAA	400

(2) INFORMATION FOR SEQ ID NO: 4458:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4458:

GAGTGCCTG TCTGGAATCT GGACTCACTG ATCTGATTCT GGAGTCGCTA TCTGATTCTG	60
AGTCGCTGTC TGAATCTGAA TCACTGTCTG AATCCGAATC GCTATCTGAT TCTGAGTCGC	120
TATCTGAACC TGAGTCGCTG TCTGAGCCTG AGTCACTGTC TGAATCCGAA TCCGGATCCG	180
GGTCTGGGGn TGGTTCGGT TCTGGGTCTG GGACTTGGTT CTGGATCTGG CGTTGGTTCT	240
GGGTCTGGGG TCTGGACTGG TTCTGGGGTC AAACGGCGGC CCTGGAGTGG GGTCTTTTCGG	300
AATnAACGGC GGAATCACCA TCAAGCAACT TnCAACAACC ATAACGAAAA A	351

(2) INFORMATION FOR SEQ ID NO: 4459:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4459:

ATCCTGCAGT TGATCAGTAT GGTGATATTA AATTAGTTAA TACGAACGCG TCATCTACAA	60
GTGAAATCAT TTACGATTTA ATCTCACATT TTAATGATGA AGCAATTGTT AATAAAGATA	120
TCGCGAGCGT TTTATATCTT GGTATCGTCG GTGATACTGG GCGATTCCTT TTTnACAATA	180
CCTCAGAACA TACTATGGAA ATTGCTGGAA AGTTAATTGG GCATGATATT GATCATATG	240
CGCTTTTAAA TAAAATGATG GAGAAGGnCC C	271

(2) INFORMATION FOR SEQ ID NO: 4460:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 283 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4460:

```
ACTGTGGATT AATATTATGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTCGACTAC      60
CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC      120
TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT      180
GATTTTGCTT CGCAnAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC      240
GCCACATGTC ACCATGCTTC CACCTCGAAC CTATnAACCT CAG                          283
```

(2) INFORMATION FOR SEQ ID NO: 4461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4461:

```
CTTCTACAAG TCCTGAATAT ACTTATGAT CTCTTCTTTC GTGTATGCAA ACTGACGTTG      60
TAATTTAAAT AACGTCTCAT CTTTCCATTG CGAATCTTGA TATTGTATAT TTTCAAATC      120
AAAGTCAACT TTATGGTTAT CAATCCACGC TTTATATGGT AATTCTCCAG CAATCGCACC      180
TTTTAAATCA TTATTTTCAA TGACTTTATT CTGTTAAAAT CAACAAnCAT AATTTCCnG      240
GATTCAATTG ACCTTTAAAA GCAACATTAC TTCC                          274
```

(2) INFORMATION FOR SEQ ID NO: 4462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4462:

```
GGCTGCTAAA AATCTTGGTA TTCACGTTGC ATCACCAGTA TTTGACGGTG CAAACGATGA      60
CGATGTATGG TCAACAATTG AAGAAGCTGG TATGGCTCGT GATGGTAAAA CTGTACTTTA      120
TGATGGACGT ACAGGTGAAC CATTCGATAA CCGTATTTCA GTAGGTGTAA TGTACATGTT      180
GAAACTTGCG CACATGGTTG ATGATAAATT ACATGCGCGT TCAACAGGAC CATATTCACT      240
```

TGnTACACAA CAACCACTTG GCGGTnAAGC G

271

(2) INFORMATION FOR SEQ ID NO: 4463:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4463:

GCGGCTCATC GCATTCATTT CTTCTCTAGC AACGTTCTAC TCTAGCGGAA CGTAATTAGC	60
TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT	120
TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC	180
AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTTTTAnTTTGAC	240
GTTTGTAGACA TAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAAAG GTCTAnTCTA	300

(2) INFORMATION FOR SEQ ID NO: 4464:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4464:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA	60
TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTTGGGC ACTGTCTCAA	120
CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG GACAGGACGG	180
GAAAGACCCC GTGGGAGCTT TTAGTGGTTA GCCTGGATAT TGGAAATTCG GGCACACTTG	240
GTTACAGGAT AGGTAAGGAG CCTTTTGGAA ACGTTGAGCG CTACTTTAnG TTGGGAGGCG	300
CTGGTnGGGA TACTTACCCT AACTGTTTTT GGCTTTTCTn AACCGGCACC ACTTATCCTG	360
G	361

(2) INFORMATION FOR SEQ ID NO: 4465:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4465:

CTGTATGTAC ACCACCAATC GGTTTAGGTT TAGCAACGTT TGTTCAAAAAG TATAAATTCA	60
ATCATTCCGA AAGAGAAATG GGTAAGGCTT CCTTCACTAT GGGACÆTTT GGTATTACTG	120
AAGGTGCTAT TCCTTTCGCA GCCCAAGATC CATTGCGCAT TATACCTGCA AACATCATTG	180
GTGCAATGAT TGCATCAGTC ATTGCAGCCA TTGGTGGTGT CGGCGATAGA GTCGCACATG	240
GnGGTCCCAA TCGTGGCTGT ATTAGGTGGG TTTTGTTTT TTTTnTTTT TT	292

(2) INFORMATION FOR SEQ ID NO: 4466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

GCAAACAAAA CAGTATTAGT AGATTATGAA AAATATGGTA AGTTTTATAA CTTATCTATT	60
AAAGGTACAA TTGACCAAAT CGATAAAACA AATAATACGT ATCGTCAGAC AATTTATGTC	120
AATCCAAGTG GAGATAACGT TATTGCGCCG GTTTTAACAG GTAATTTAAA ACCAAATACG	180
GATAGTAATG CATTAAAnAGA TøAGCAAAAT ACAAGTATTA AAGTATATAA AAGTAGATAA	240
TGCCnCTGAT TTATCTGAAA GTTACTTTGT GGAATCCCGG AAACCTTGAG GGTGGCCCCT	300
AATAnTGG	308

(2) INFORMATION FOR SEQ ID NO: 4467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4467:

AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCATAATAA TÆCAGTATA TCGGGAAGAC	60
AGGATTTCGAA CCTGnGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT	120
CCCGTATAAT TAAngCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA	180
CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTTATT GAAAATAGTG CCGAGGACCG	240
GAATCGAACC GGTACGTGAT CACTCACCGC A	271

(2) INFORMATION FOR SEQ ID NO: 4468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4468:

```
TGTGTTAGGT ATTACATCAT CACATTTATC TCGTCAAAG TCCAGCTGTC GATAAAGTTG      60
TAAACTGTAA AAACGCAATT TCTGAATTAG AAAATGATAA ACGTAAAGCA GTAAGTGCTG      120
AAGAnTATAA AAAAGCTGAC GACATTCAAA ATGAAATCAA ATCATTACAA GATAAATTAG      180
AAAATAGTAA TGGTGAACAT ACTGCTGTTG CTACAGTTCA TGATATTTCA GATACTATTC      240
AACGATTAAC TGGTATTCCA GTTTCTCAAA TnGATGATAA CGnTATTGAA CGTTTAAAAA      300
ATATTT                                     306
```

(2) INFORMATION FOR SEQ ID NO: 4469:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4469:

```
GGTTTATTAA CAGCATTCTT ATCAGCATTT GTAAGTGTTA TTGTTTATAA CTTCTGTGTG      60
AAGCGCAATA TTACAATTAA AATGCCGAAA GAAGTACCGC CGAATATTTT ACAAGTATTT      120
AAGGACTTAA TTCCATTTTC AGCGGTAATC ATCATTCTTT ATGCATTAGA TTTAGTCATT      180
CGCAACAGCT TTAAATCAAA TGTAGCGGAA GGTATTTTAA AATTATTCGA ACCATTATTT      240
ACAGCAGCAG ATGGATGGGT TGGTGGTCAC CATTAAACnT TGGGnGCnTT TGCATTAATC      300
CTGGGTTTGT AGGGTAATCC ATGGGTCCG                                     329
```

(2) INFORMATION FOR SEQ ID NO: 4470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4470:

```
AACTGGGTGA TAAGGTCTTG TTCGAAAGGA AACAGCCCAG ACCACCAGCT AAGGTCCCCA      60
AATATATGTT AAGTGGAAAA GGATGTGGCG TTGCCAGAC AACTAGGATG TTGGCTTAGA      120
AGCAGCCATC ATTTAAAGAG TCGTAATAG CTCCTAGTC GAGTGACACT GCGCCGAAAA      180
```

TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTCCTTGGACAAT GGTAGGAGAG	240
CTTCTAAGGA CTTGAAGCTG ATCGTAAGAC TGTGGAGCGn TAGAATGAGA TGCCGTGTGA	300
TAGnAAAGAC GGTGAGATCC CTCCACCGTT GACTAAGTTC CAGAGGAAGC TCTCCGTCGG	360
GTTATCCGGT CCTAAGnGAG GCCGACAGCT AGGCATGGnT	420

(2) INFORMATION FOR SEQ ID NO: 4471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4471:

TCATTTTtag AAATATTATC TTTTCCACAA ATCATTtGAT ATAAAGTGCG ATCATTtGCC	60
GCGAGtGCTG CCATTGACAC TAGCTGTTGC GTATCATTTT TGGCTAGCAC TTCGGGATAC	120
TTTCTTAGCT GAACAGTTAG ATGACCTAAT TGATCTTTGA AAATATCATT ATCTTGACCC	180
ATATATGACC ACCAAGCTGT TTCATCACAA ACCATGACAT ACTTAGCTAG TGCTTCATCT	240
TTTTCTATAA GCTGACGTAA TAATTGTCTG CTTGTCCTCC GTTTTnCATG TACCGCGAGG	300
CGTAAnCTTA AAGGGCCCAA GGnCG	325

(2) INFORMATION FOR SEQ ID NO: 4472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4472:

CCCGTCTTTC GCTACTCACA CCGGCATTCT CACTTCaAG CGCTCCACAT GTCCTTACGA	60
TCATGCTTCA ACGCCCTTAG AACGCTCTCC TACCATTGTC CAAAGGACAA TCCACAGCTT	120
CGGTAATATG TTTAGCCCGG TACATTTTCG GGGGCAGTGT CACTCGACTA GTGAGCTATT	180
ACGCACTCTT TAAATGATGG GCTGCTTCTA AGnCAACATC CTAGTTGGTC TGGGGCAACG	240
CCACATCCTT TTTCCACTTT AACAnATATT TTGGGA	276

(2) INFORMATION FOR SEQ ID NO: 4473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4473:

```
AATTTnCCAA AAAATTCAAA TGGCTCATTT ACCAAAAGGT AAACCTCCGC CTTTAAnTTT      60
CTTaATGCAT kGTCTAACAA cCGCTTTCTT TAAAaAATA GATTGTCAAG CGCTCGCATA      120
AGCAATATCA CTTTAACCAA AAAATATTTG AATGTTAAAT AAACATTCAA AACTGAATAC      180
AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG      240
AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTtGTTA CGACTTCACC CCAATnATT      300
TGTCCCACCT TCGACGGGCT AGCTCCGAAA AGG                                     333
```

(2) INFORMATION FOR SEQ ID NO: 4474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4474:

```
TATAAAATAG CAACGTTATT CCAATTATCT TAATGGTTAT CTTATCCTCA ACTAAATTGG      60
AGGAATCACT ATGACAATTA ATAAAGTAAC CGTTCTTGGC GCAGGCACAA TGGGCGCTCA      120
ACTGGCAGCA CTTTTTGTGA ATGCTGGACT TAAAGTAAnA CTATTAGATA TTGTAGTGG      180
CAAAAACGAT CChAATCTCA TTGCGAAAAA ATCTTACGGT TAAATTACAG GTAAGAAACG      240
GCCGCTACTA TTCGnCTTAA ATCTAGCGGT CATTTACCAT ATGGTATTTT GATGTGCTTG      300
GTAAATGTGT GCTGTTTGAT ATCGA                                           325
```

(2) INFORMATION FOR SEQ ID NO: 4475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4475:

```
TAAGTGGGC AACATTTGCT TGTTTTGGTT ATGGTTGGCA CATTGATGTC GGCATTCATA      60
CAATACATCT AGTATTATCT GGTATTTTTG ATCGTTATCC AAAGTTAAAT AATGATTATT      120
GGACATTGGG GTGAGTTTAT CCCATTCTTC TTAGAAACGT ATGGATGAAG CTTATTCGCT      180
GACATTTnAC CACCCTGTAA GCTATACTTT AAAATAATT TTTAATCACA CCGAGTGGCA      240
```

TGTTAACGAG CCACAGTTTG ATTTAGTCAA GAAGnAGAGG TATTGTAGAn TCTTATGCGC 300
 TGATATCC 308

(2) INFORMATION FOR SEQ ID NO: 4476:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4476:

ATGATATGCT GTATATCCCA CCAGCGCCTC CACGTAAC TA GCGCTCACGT TTCAAGGCT 60
 CCTACCTATC CTGTACAAGC TGTGCCGAAT TnCAATATCA GGCTACAGTA AAGCTCCACG 120
 GGGTCTTTCC GTTCCTGTCG CGGGTAACCT GCATCTTCAC AGGTACTATG ATTTACCCGA 180
 GTCTCTCGTT GAGACAGTGC CCAAATCGTT ACGCCTTTTCG TCGGGGTCGG AACTTACnCG 240
 ACAAGGAATT TCGCTACCTT TAGGACCGTT ATAGTTACGG 280

(2) INFORMATION FOR SEQ ID NO: 4477:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4477:

GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG 60
 CTTACTCATT TAGCTCTACT AAAC TCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 120
 GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TTTTACTTT TTATTTTGAC GTTTTAGACA 180
 TAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA 240
 ATTGGGCTAC CATCGnCGCT AAAGACCTTT CTTGACTTG 279

(2) INFORMATION FOR SEQ ID NO: 4478:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4478:

GAGGATCCCG GAATGTTGAA CCCATCACTG ATTCTGGTTC ATAATTATCC ACATCCATA	60
ACGTAAATC TAAAGCGTGT GTACCGATAT CGATTAAATGG TCCTCCACCT TGAGCTTCTT	120
CGTCTAGAAA GACACCCCAT GTTGGnACTG CTCGACGACG AATGGCATGT GCCTTTCCGA	180
AGTAAATGTC TCCTAAGTCG CCACGTTGCG CTGCTTGATG TAAAAATTGA CTATCTGCTC	240
GGAnACGATT TTGATAACCT ATTGTTAATT TT	272

(2) INFORMATION FOR SEQ ID NO: 4479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4479:

GAAATTGGGA ATCCAATTTT nCTTTGTTGG GGCCCATCCC CAACTTGCAC ATTATTGTAA	60
GCTGACTTTT CGTCnCTTAC TGTGTTGGGG CCCTCACCCC AACTCGCATT GCCTGGTAGA	120
ATTTCTTTTC GAAATTCTCT GTGTTGGÆC CCCTGACTAG AATTGAAAAA AGCTTGTTAC	180
AAGCGCATTT TCGTTCAGTC AACTACTGCC AATATAACTT CGTAGAGCAT AGAATATTGA	240
TTTATGTCCC AGCCTGAGTT AATT	265

(2) INFORMATION FOR SEQ ID NO: 4480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4480:

ACATAGAAAT GCCACTTTTA CAAACAAATG AATATTCGTC TTTTACÆC ATTACGCATA	60
ATAAAAGAAG CTAAGCAACA TGTAACCGT TGTCACTTAA CTTCTTGTTT TTCCGATGAC	120
AGCTTCTATT TAGAGAATGT CATGATTATT TTATATTCAC TTCAATGTTA TCAATATTAG	180
TGCCATCTAT GACGTCTGCC ATACGATGCT CTGGCAGTTT TTTGGTGTA ATTCAAACGT	240
ATATTCCCAC CGTTTTTATT TAATAACGTT GTCCnGGACC CATGTACCGT AAGATATGTT	300
TTCATAGTGG TTCCAATTAA ACCAnTCTTC AGGAACCTCn TAG	343

(2) INFORMATION FOR SEQ ID NO: 4481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4481:

ACTGCGGCAA TAGCAGCAGC ACCACAAACG GCCTGTGTCC GGACACCTAG GTAATAATGC	60
GCATGTTTTT GTCACCATGC CAAAGTTTG TTGACAAAGA GCATCATTAC AATACTGGAA	120
AATAACGACA CCTACATCGA TGGCTAATAG TTTACTACCT TGACCGATAA TATCGAATAT	180
ATTGAGTTTA AGTCCATATA GGATGATTGC AAATCTTAAT AAATATTTAG ATGAAAACGT	240
AATACCTGAG CTATATTGnT CAGGATATCC TCTAGAGTGA CGATAnAG	288

(2) INFORMATION FOR SEQ ID NO: 4482:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4482:

GAGGCATCCC CGGGCCTTCC TTCCCAACAG TCGCTTCAAA GTTTGGTGGT AAACCTGnTA	60
CATCAAATTA TCGGTGCTAC TGTnAGGTAC GTGTAATCTT CGCTATTTTA TTAGCCGTAT	120
CACATCAAGT GGCTTCCCTA CTGGAACCAA TTTGCTATTC GCCTTATTAT CAGGTGCAGG	180
ATGGGGATTC GGACAAATCA TTACATTTAA AGCGTTCGAA TTAGTCGGCT CATCTCGTGG	240
CCATGCCAGT CACAACAGCA TTCCAATTAT TAGGCGCATC TTTATGGGG	289

(2) INFORMATION FOR SEQ ID NO: 4483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 264 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4483:

AATCAAAAGT GCACATTATT AAAATATCAA TTTCACTC AATGCGGCTC ATCGCATTCA	60
TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT CCTCGCTAAG	120
AACCTTTCTT GACTTGTGAC AATCGCTTGC TTCTTTCTC TCCTTCGGCT CTCGCTTACT	180
CATTTAGCTC TACTAACTC GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTnC	240
ACTTCGCCAA GnCATTTTTTC TTG	264

(2) INFORMATION FOR SEQ ID NO: 4484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4484:

```
CTGTACCACC TATAATCGTT TTAATCGATT GGGGGACGCA TAGGATAGGC GAnGTGGCGA      60
TTGGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC      120
TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA      180
nAAGCCTCTA GATAGAAAAA GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG      240
AATTCTAAGG TGAGCGAGCG A                                          261
```

(2) INFORMATION FOR SEQ ID NO: 4485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4485:

```
ATGCAGCTAT TATTTTTGAC AGATTCCATA TCGTTCAACA TTAAATAGA GAACTTAATA      60
AGTATCGTGT ACAAGTTATG AATGAATACC GTAATAAAAA AGGACCTGAT TATACAATTT      120
TTAAGAATAA CTGGAAAGTC CTATTGATGG ATACTAGTAA AACCATATTT AGTAAATACA      180
GATGGAnTAA ATCTTTTAAG GCTTATAAAC GCTCATCTGA CATTGTAGAn GTCATGCTTT      240
CAAAAGACGA TATACTACGA C                                          261
```

(2) INFORMATION FOR SEQ ID NO: 4486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4486:

```
AGCAACATGA TGCACTTCTC GTGTCTCACC AGATTTAGCG ACTAAACTTG TAGACATACG      60
TAAATCTGCT TTAATAAGTA ATnATGCAC ATGACTTATT GCGAGTAACA TCGGCATTGC      120
AAAGCCATTG CTATCAACTA ATCCACTATC ATCTAACACT AGAnTTTGAG CGCCTTGCTT      180
```

TACAGCATTG ACTGCTTCTC GGCCTAATGC TTCTAACGCA TCTTCCAAAT CCCCTTCATA 240
TACCGTTGAT AAATAAGTTA 260

(2) INFORMATION FOR SEQ ID NO: 4487:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4487:

ATGAGGTGCA TAGGGATAAA ACAGnnAGCA GCAATTTGTC GCTATTTGTA AATTGTATCC 60
 TGGCTTAAGT TGCCATTTT TCATATGGTC TTCCTTCATT CTCATAAAAG TTGCATCATG 120
 ATCAGTTTTA GAAAAGCTAT TTCTATCTTT AAGAATCGAT TTTTGTTCCT CATATTTATT 180
 TTTTCTTTTCG GAATAATCAT CAAATTTATT TTTGAACTTC TTAATCTTAG TTCTTTTTTA 240
 CGGGTCTGTT TTCCAATTTG AGTACTATCC TCGTTCCCn ATAGAATGAA TTAAACCTT 300
 CCGATTTTCCT TTAAnC 316

(2) INFORMATION FOR SEQ ID NO: 4488:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4488:

CACTTTTACT GCTAAAACGT CAATTGTTGA TGAGTCGTGT TTTATCTCAA GATGTGTTAC 60
 TCAAAAAGTT ATAGAAGAAG CTAATAAGT TAAACAGAG ATTGATACTG CCAGAAGAT 120
 ACTGTATCTC TCCATCTACT GTAAGTCCGT ATTAGAACTA AAGCGGCTAA TTCATTACGA 180
 ATTAAACCCT TTAATTGTTT GCCAGACACA TCGCTATGGA TGAATTTAAA GCGTnAAAAAT 240
 GTACTGGATC ATGAGTTCAT TTTTATAGnT ATGTACnCAT GTGTATAGTA TTTAGAAATA 300
 GACTCAA 307

(2) INFORMATION FOR SEQ ID NO: 4489:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4489:

TTGGCAAATG TCATATAACT AGTAACATGA TCATCGACAT CAAATTTAGT ATGATCAAAT	60
GTTCCCAAT CATTAATTTG ATTCGGTTGT TTGCTCAATT GATTATATGT TTTTCCTAGC	120
ACTTCATGCG GCACCATATC TTTACCTAGT AGCCACAA AGATAAGTCT AACAAGTGGC	180
ACCATAATCG ATAACTACC GCCACCTGCA CGCTTATGGT AAAACACCCA GCCAGCACTT	240
ACGCTACGCA TCGCTGTACA CGTGCTACTA AGGTTACCAC CACACTGATT CAATGCTTTT	300
TAGCAGTATG CCACnCCGn GACGATATGG TAGCGACGTA AnAA	344

(2) INFORMATION FOR SEQ ID NO: 4490:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4490:

CCCAACCGGC ACATTGTTGT AAGCTGACTA TATGTCACTT CnTGTGTTGG GGCCCCTGTC	60
TTCGACTGGC ACTGCTCCCT CAGGAGTCTC GCCATTAATA CTACGTATTA ACATGTAATT	120
TTACTTTTAA ATACTTTAAA AAAATAAGAC ACTTTGGTCC AACTTAAGCC AGGGATACAA	180
TTTACAAATA GCGACAAATT CTCAATTTGT nTTATCCTAT GGACCTATTT CAAAACCCAA	240
CAGGTACTnA GTAACCTTTGA ATTCCATTTT TTAACAATGG ATTGCAAAAT GACCTTACGG	300
TTCATTTGAC CGG	313

(2) INFORMATION FOR SEQ ID NO: 4491:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4491:

AGGTCTGACT CTAGAGGATC CCCGATGAGT TAAAGAAAA ATATCAAACA CCTGAATTAT	60
ATTTTAAAGC TTGGCAAGGT TTTTACCACG AGGTTACAAA TGAGCCAGAA CGTGATGAAG	120
TAATGCGTTA TATTCTGACT TTCTTAAATA ACAGCGTCAA TACAATGGGC TTTATTGTTG	180
AAGATGACGA AATTGTAGAA ATTTAATATT CTAAAAAGGT TGGGACATAA ATCCCTAAA	240
AACAGCAGTA AGATAATTTT CCATTAGAAA ATATCTTACT GCTGTGCnA A	291

(2) INFORMATION FOR SEQ ID NO: 4492:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4492:

GCCGTCTCAG CCTTGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAAATACT	60
ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACTTAAAAAA ATAAAACACT TTGCCCAACT	120
TACACTACCA ATAGAAACTG CTGTTAGAAT TCCTCAAAT GATATTTTCGC GATATGTTAA	180
TGAAATTGTT AAAAAGATAG CTGATAGCGA GATTCGATGG AATTCAGACA TCATCGTGGG	240
CGCAACATCC TATCATCTAA AAATGATGTT AAAAATCACC TGCATATTGC ATATACTGCA	300
ATCTGGAATT TTCTGGGCCG TGAGAATGAG AAATnGAC nTCATGAACA GTGATTGCGA	360
ATGGATGTGG GTTAAGCTnC AAGATTCAAA CACCTTGCnT	400

(2) INFORMATION FOR SEQ ID NO: 4493:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4493:

TGATCCAGAG ATTTCCGAAT GGGGAAACCC AGCATGAGTT ATGTCATGTT ATCGATATGT	60
GAATACATAG CATATCAGAA GGCACACCCG GTAGAACTGA AACATCTTAG TACCGGAGG	120
AAGAGAAAGA AAATTCGnTT CCCTTAGTAG CGGCGAGCGA AACGGGAAGA GCCCAAACCA	180
ACAAGCTTGC TTGTTGGGGT TGTAGGACAC TCTATACGGA GTTACAAAGG AnGACATTAG	240
ACGAATCATC TGGAAAGGTG AATCA	265

(2) INFORMATION FOR SEQ ID NO: 4494:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4494:

CATTACTAAA AAAGATAATC AAGGTATGAT TTCACGCGAT GTTTCAGAAT ACATGATTAC	60
TAAGGAAGAG ATTTCTTGA AAGAGCTTGA TTTTAAATTG AGAAAACAAC TTATTGAAAA	120
ACATAATCTT TACGGTAACA TGGGTTCAGG AACAATCGTT ATTAAAATGA AAAACGGTGG	180
GAAATATACG TTTGAATTAC ACAAAAAACT GCAnGAGCAT CGTATGGGCA GACGTCATAG	240
ATGGGCCCTA TATTGATACC ATTGGAGGTG AATnTAAATA ACCATGCACT CTC	293

(2) INFORMATION FOR SEQ ID NO: 4495:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4495:

ACTTACAAAG TTCTGTGAAC CAAGTACCAT CAACTGCTGG TATGACGCAA CAAAGTATTG	60
ATAACTATAA TGCGAAGAAG CGTGAAGCAG AAAGTAAAT AACTGCAGCTCAACGTGTTA	120
TTGACAATGG CGATGCAACT GCACAACAAA TTTGAGATGA AAAACATCGT GTGCGATAAC	180
GCATTTAACA GCATTnAAAC CAAGCGAAAC ATGAnTTTAA CTGCAGATTA CACATGCCTT	240
AGGAGCAAGC AGTGCA	256

(2) INFORMATION FOR SEQ ID NO: 4496:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4496:

GTCATCAGAA ACCCTTGTC AACAAGGCTT GTATTTTTTA TACTTATTTT TTAAATTAAA	60
TTCATCATTA TCTAATTTAA AACAATATAC TAAACGTTTC ATAATTATCG CCTGTACAAT	120
ACGCACAAAA ACATGTCTTG AAACGCCTTT CATTACTCTA AnATACCCAA TATACTTTTT	180
ATATCGTTTC GATTCTGAGT ATTTCTGAGC ATTTTCTGCA TAnAAATAAA CGTGTTTCAA	240
GGCAATATAT TGCA	254

(2) INFORMATION FOR SEQ ID NO: 4497:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4497:

AATCGGCTGT CTGATTCTGA ATCGCTATCT GAGTCCGAAT CGnTATCTGA ATCCGAGTCG	60
CTATCCGAGT CTGAGTCGCT ATCTGAATCC GAGTCACTGT CGGAGTGGGA ATCACTATCT	120
GAATCCGAAT CACTCGCTGA ATCCGAATCA CTGTCTGAGT CTGAGTCACT GTCGGAATCT	180
GAGTCACTGT CGGAATCTGA ATCGCTATCT GAATCCGAAG TCACTGGTCG GGAATCTGAG	240
TCACTGTnGG AATCTGAATC GCTATCTGA	269

(2) INFORMATION FOR SEQ ID NO: 4498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4498:

CACCCCGGCA CTATAAAAT GGAGCAGAAG ACGGGATTCTG AACCCGCGAC CCCAACCTTG	60
GCAAGGTTGT ATTCTACCGC TGAAGTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC	120
CCACGCCGTA AGCTTAGnAT ACCTCAAGTC TAGTGCGTCT GCCAATTCCG CCACACCCGC	180
AAATGGTGAG CCATAGAGGA TCGAACCTC TGACCCTCTG ATTAAAAGTC AGATGCTCTA	240
CCAAGTGGC TAAATGGCTC TnTnAGGTGC CGG	273

(2) INFORMATION FOR SEQ ID NO: 4499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4499:

GTAAGTAAAC GCATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT CACGGCAATT	60
TAGGGATTAA TATCAAGAAT GACGCTATTG CATCGAATGG TATATCACA CCAGGTGTTT	120
TTGAATATTA AAAGGAGAAT CGATTTGAAG TGCnnCATAA GACAATACGG ACTTATCAAA	180
TCAACGAAGG AGACAAACTA GCTCAATTGG TTATCGTGCC TATATGGACA CCTGAACTAA	240
AGCAAGTGGA GGAATTTCGAA GTTGTTCAnA CGTGGAGAAA AGGCTCGGAG AGCGGGTGAA	300
AGCATCTTAG TCGA	314

(2) INFORMATION FOR SEQ ID NO: 4500:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4500:

ATTGTAAGGC TATCATGTCA AAGATTATAA CAATAAATCT GGTGAGATT TGGTGGCGGG	60
GCGATGGAAG CTATCTATTT GACCATCCAT TTGGCAAAGG TTTGGGAGTT ACACAGGTGG	120
ACTTAACTTT AATGGCGGTC GTCACATATGG TATCGACTTT GGTATGCCTA CAGGAACGAA	180
CCATTTATGC TGTTAAAAGG CGGTATAGCT GATAAAGTAT GGnCTGATTA CGGTGGCGGT	240
AATTCATAC AAATTAGGAC CGGTGCTAAC GAATGGAnCT GGTATATGCA TTTATCTAnG	300
CATT	304

(2) INFORMATION FOR SEQ ID NO: 4501:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4501:

TTCCTTCATT CTCATAAAAG TTGCATCATG ATCAGATCAG TTTTAGAAAA ACTATTTCTA	60
TCTTTAAGAA TCGATTTTTG TTCTTCATAT TTATTTTTTC TTTCGGnATA ATCATCAAAT	120
TTCTTTTTGA ACTTCTTAAT CTCAGTTATT TTTTACGGG TCTGTTTTCT AATTTGAGCA	180
CAATCTTCGT TCTCAATAAG AATGATTTAA ATCTnCGATT TCTTTATCTA AATGGACTAC	240
CAATTAAATC TAT	253

(2) INFORMATION FOR SEQ ID NO: 4502:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4502:

AGTTCGGTCC CTATCCGTCG TGGGCGTAGG AAATTTTnGA GGAGCTGTCC TTAGTACGAG	60
AGGACCGGGA TGGACATACC TCTGGTGTAC CAGTTGTCGT GCCAAngCAT AGCTGGGTAG	120

CTATGTGTGG ACGGGATAAG TGCTGAAGAT GCTTAAGCAT GAAGCCCCC CAAGATGAGA	180
TTTCCCAACT TCGGTTATAA GATCCCTCAA AGATGATGAG GTTAATAGGT TCGAGGTGGA	240
AGCATGGTGA CATGTGG	257

(2) INFORMATION FOR SEQ ID NO: 4503:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4503:

ATACGTTTAA TACACAAAAA ACTGCAAAGC ATCGATGGCA GACGTCATAG ATGGCACTAA	60
TATTGATAAC ATTGAAGTGA ATATAnAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA	120
TCGGAAAAAC AAGAAGTTAA GTGACAAGnT TTACATGTTG CTTAGCTTCT TTTATTATGC	180
GTAATGATGT AAAAAGACGA ATATTCATTT GTTTGTAAAA GTGGCATTTC TATGTCTTAA	240
AAGTGACGAA ACTTCAAATG TGCCAAGTGT	270

(2) INFORMATION FOR SEQ ID NO: 4504:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4504:

TACCTTGACC GAAGTTCTTA CCTACATCAC CTAAATTAAT GACATGTCCA CCAGTCATAT	60
ACTCTAATCC ATGGTCGCCG ATACCTTCAA CGACAACATC TACACCACTA TTTCTAATAC	120
AGAATCTTTC TCCTGCACTA CCGTTAATAA ATGCCTTACC ACTTGTCGCA CCATAGAATG	180
AGACGTTACC AGCAATAATT TCATTTTGTC GTTCTTCAAA AGGTGCTTTG ACAATGACCG	240
TACCACCnGn T	251

(2) INFORMATION FOR SEQ ID NO: 4505:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4505:

AGAAGTTAAG CTCCTTAGCG TCGATGGTAG TCGAACTTAC GTTCCCGCTA GAGTAGAACG	60
TTGCCAGGCA AATGACAAAT CGGAGAATTA GCTCAGCTGG GAGAGCATCT GCCTTACAAG	120
CAGAGGGTCG GCGGTTTCGAA CCCGTCATTC TCCACCATTT ATTCTTAGAT ATAGCGGCC	180
TAGCTCAATT GGTAGAnCAC TGACTTGTAA TCAGTAGGTT GGGGGGTCAG TCCTCTGGCC	240
GGCACCATCT TTTGnCCATA	260

(2) INFORMATION FOR SEQ ID NO: 4506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4506:

TTCTTTAGTA GATACTAAGG CGTTATTAGA CGCATTAGAC AATGGTGTGA TTAAAGGTGC	60
AGCACTTGAT ACGTATGAAT TTGAACGCAA ACTTTTCCCA AGTGATCAAA GGGGCAAAC	120
ACTGAACGAT CCATTGTTAG AATCGTTGAT TGACAGGGAA GATGTCATAT TAACACCACA	180
TATTGCGTTT TATACTGAAG CTGCAGTTAA AAATCTATTG TCGTGCATTA GGTGCAACAT	240
TAGGTGTATT GCAGCTTGGG GAACTTnGnT ACnGTAAAT TTAAATCGG CTGTGGGTAT	300
TTTGnTTTT GGG	313

(2) INFORMATION FOR SEQ ID NO: 4507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4507:

GnCAATACGG CCAATTCCTA AGATTGCTAC TTCTGGGTGG ATTGATAACT GGAGTGAACC	60
ATTGTCCACC AGCTGnAACC GATATTACTG ATTGTGCATG TAGCACCTTT CATTTCATCG	120
GCTGTTAATT TACCATCACG TGGCTTTAAC AGCTAATTCA TTAATTTTCAT CTGAAATTTG	180
GGAAAATAGA CTTACGGATC AGCATGTTTA ACAACAGGTA CTAATAATCC TCTATCAGTG	240
TCTGCTGCAA TT	252

(2) INFORMATION FOR SEQ ID NO: 4508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4508:

CATCGAACCA GATGTACTCG CACTTGTTGA GTCTGATGTT GAATCACTAA CACTATCAGA	60
TAATGACGTT GAATCACTCA TACTTGTTGA TGTACTTGTC GAAAGCGACA TACTTTGTGA	120
ATCACTAGTA CTTGTACGCA TCGAAGTACT AGTTGAAGCT GATGTACTAC GAGAGTCACT	180
TGTTGATGTT GATGTACTTG CTGATCCTGA TGCACCTGTA CTTCTTGATG TGCTTTGTGA	240
ATCGGATTTT GCTCGTGcT GGTACTnG	268

(2) INFORMATION FOR SEQ ID NO: 4509:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4509:

CGAGAGTGCG TTAATTGGT TACTGCTATC ACgTAAGGGG CGGAAACCCC CTAACACTTA	60
GCACTCATCG TTTACGGCGT rGACTACCAG GGTATCTAAT CCTGTTTGATCCCCACGCTT	120
TCGCACATCA GCGTCAGTTA CAGACCAGAA AGTCGCCTTC GcCACTGGTG TTCCTCCATA	180
TCTCTGCGCA TkTCACCGCT ACACATGGAA TTCCACTTTC CTCTGCTGGC ACTCAAGTTT	240
TCCAGTGTCC AATGACCCTC CACGGTTGAG CCGTGGGCTT nCACATCACA CTTAnA	296

(2) INFORMATION FOR SEQ ID NO: 4510:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4510:

TTACTACTTA CTGAGTGACC TGTACCTGCT TTCGGAGTAA TTGTGATTGA TGAATTTGGT	60
TTTATAGTAT TGGCATTGAA CGTCACTTTA CCAGTTTGTG CATCTAACGT TACATAGTCA	120
GGCTTATTTC CAATTGTCCA TTGnTTATTT TGACCACGAA CAACATTAAT TGTCTTACTA	180
TGTTGCTGCA CCATTACCCA CTTnTtAGT GTAAGCAATA TCCATTGCTT GAGTTGGGAT	240

TAATTAAATG GTCCTGA

257

(2) INFORMATION FOR SEQ ID NO: 4511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4511:

AAAATCACAT CAGCCTGCAT TAACGACGTC GTTAATTTAT ATACATCTCC TGTAGTATCT	60
AGATAATTCT TTCCAACGCT AAATTCTAAT TCAAGTTCTC GTAAATCAT CAACTCTATT	120
TGATGTCCCT CATTGATGAC TTCTAGTTCA TTTTAAAT CATCCATAGC AATTCTCGTT	180
TTAGAACCTA CTGTGGAACC TGACAATAAT ACAATATTCA nGAnGACGCC CCTCCTATTT	240
TGATAAATGC	250

(2) INFORMATION FOR SEQ ID NO: 4512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4512:

AGCTGGnTTC GAACCAACGA GTGACGGAGT nAAAGTCCGT TGCCTTACCG CTTGGCTATA	60
GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTGAACTG CCGAACCCGA AGAGCGGATT	120
TACAGTCCGC CGCGTTTAGC CACTTCGCTA CCCCTCCAGC TTATTCATAT AATTTAATAA	180
TCAAAATGGT GGAAGAATGA CGGTTCGAA ACCGCCGACC CTCTGCTTGT AAGGCAGATG	240
CTCTCCCCAG CTG	253

(2) INFORMATION FOR SEQ ID NO: 4513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4513:

GnCGACCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA CGTTAACATG	60
nAAGTTACGT TCTTTTATAA AAAGATTTAA ACGCGTTATT AECTTGTC AGTGTCTTT	120

CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG	180
TTTTGCTTGG TTAAAATCTA TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG	240
GTGGAGACTA GC	252

(2) INFORMATION FOR SEQ ID NO: 4514:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 244 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4514:

GTCATTGAAT ATGGAAACTT TAGAATTACA AGGCGCTAAA TTACGATACC ACCAAGTCGG	60
ACAAGGACCC GTGCTCATCT TTATTCCTGG TGCAAACGGT ACCGGAGACA TTTTCTGCC	120
TCTTGCAGAA CAGTTAAAG ACCATTTTAC TGTTGTAGCC GTTGATCGTC GTGATTATGG	180
AGAAAGCGAG TTAAGTGAAC CACTCCCTGA TTCCGCTTCA AACCTGACA GTGATTATCG	240
TGTC	244

(2) INFORMATION FOR SEQ ID NO: 4515:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4515:

TATTAGGCAA ATCCGGTACT CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT	60
TCGAGTCGTT GATTTACAC TGCCGAGAAA AGCCTCTA TAGAAAATAG GTGCCCCGTAC	120
CGCAAACCGA CACAGGTAGT CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA	180
AGGAACTCGG CAAATGACC CCGTAACTTC GGGAGAAGGG GTGCTCTTTA GGGTTAACGC	240
CCA	243

(2) INFORMATION FOR SEQ ID NO: 4516:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 4516:

ACTAGTCGAG TGACACTGCG CCGAAAATGT ACCGGGGCTA AACATATTAC CGAAGCTGTG	60
GATTGTCCTT TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG	120
ACATGTGGAG CGCTTAGAAG TGAGAAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC	180
CCGTCCACCG ATTGACTAAG GTTTCCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT	240
CCCTAACCT GAGGCCGCAA nnGTAGG	267

(2) INFORMATION FOR SEQ ID NO: 4517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4517:

TTGAATCTGA CGAAACGAGA AAAGAGCGCA ACGAGTTTAG TAGAGCTAAA TGAGTAAGCG	60
AGAGCCGAAG AGAGGAAAGA AGCAAGCGAT TGTCÆAAGT CAAGAAAGGT CTTTAGCGAC	120
GATGGTAGCC AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAAAAA ATGGGATGCG	180
ATGAGCCGCA TTGGAGACCG CAGTCCTnTn TnTTTTTTTA TGGCCTTAAA ACGTCAAAAT	240
TAAAAAGTTA AACACAAAGA AAATGGGCTT TGGCGAGTGG AAACGTTTTG AATCTGGACG	300
GAACGAGAAA GAGCGCACG	319

(2) INFORMATION FOR SEQ ID NO: 4518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4518:

GGTATAATAG ATGACTATGT ACTATTTCCG GTACATCCTT GGCAATATCA GCATATTCTG	60
CCGAACGTCT TTGCGAAAGA GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAATTT	120
GGAGATTATC TGTCGTCTTC AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC	180
CATGTCAAnG TACCATTTGC AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GnCTACGGTT	240
ACATGAAAAA CGGGGAACA	259

(2) INFORMATION FOR SEQ ID NO: 4519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4519:

ATAGGGTGTT GCTGAATAGG GCGTTTAGTA TTGGTCGTA CCGnnAACCA GGTGATCTAC	60
CCTTGGTCAG GTTGAAGTTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA	120
AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGG AGATAGCTGG	180
TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGA TTATTGGAGG TAGAGGATG	240
TTTGGACGAG GGG	253

(2) INFORMATION FOR SEQ ID NO: 4520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4520:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT	60
TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT	120
CTCAACTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCnACC ATCGTCGCTA	180
AAGACCTTTC TTGACTnGTG ACAATCGCTT GCTTCTGTCC TCTCCTTCGG CTCTCGCTTA	240
CTCAT	245

(2) INFORMATION FOR SEQ ID NO: 4521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4521:

GGGCCTAAGT GGA CTGGAAC CACCGACTC ACGCTTATCA GGCGTGCGCT CTAACCAGCT	60
GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA ACTGAATACA ATATGTCACG	120
TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG	180
CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TnCCACCTT	240

(2) INFORMATION FOR SEQ ID NO: 4522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4522:

nATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGT TGATGGCGTG	60
CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTTAAGCAG TAAATGTGGA	120
GCCGTAGCGA AACGATGTCT GAATAGGGCG TTTAGTATTT GGTCGTAGAC CGAAACCTGG	180
TGATCTACCC TTGGTCAnGT TGAAGTTCAG GTAACACTGA ATGGAGGACC GAACCGACTT	240
ACGTTTGAA	249

(2) INFORMATION FOR SEQ ID NO: 4523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4523:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG	60
GGATGGACAT ACCTCTGGTG TACCAATTGT CGTGCCAAng CATAGCTGGG TAGCTATGTG	120
TGGACGGGAT AAGTGCTGAA GATCTnAAGC ATGAAGCCCC CCTCAAGATG AGATTTCCCA	180
CTTCGGTTAT AAGATCCCTC AAAGATGATG AGGTTAATAG GTTCGAGGTGGAAGCATGGT	240
GACAGTGG	248

(2) INFORMATION FOR SEQ ID NO: 4524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4524:

AACGTTAAGA TCCCTATTAA ATTATCTTAG GAATCATCAT GGGCATTAT GATGTCTTAA	60
AGCTGGATAT CGACATACTT ATATATGGTT ACGGTGTCCC ATGGCTTACA TATTTTATA	120

AAATTAGTAA TCTGAATCTG CTTCTAAACC TTGTCATAAT TTGA _n CGGCT GTGGCTCG _n A	180
CCAATACGGG TCGGACCTGC TT _n AACCATT TTATTGGAAA TCTTCTAAAT TACGGACGGC	240
ACCCGGATGC TTTTACTTCT ATATCAGCAC CTACTGTATC TTTCATTAAT TTAACGGCTT	300
CTGCAGTCGG ACCGGCAACT GCAAAA	326

(2) INFORMATION FOR SEQ ID NO: 4525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4525:

AAGAGCACCC TTCTCCGAGT TACGGGGTCA TTTGCCGGTT CCTTAACGAG AGTCGCTCGT	60
CACCTTAGAT TCTCATCTTG ACTACCTTGT CGGTTTGCGG T _n GGCACCT ATTTTCTATC	120
TAGAGGTTTT CTCGGCATGT GAAATCAACG ACTCGAGACA CAATGETTC TCCCATCACA	180
GTCAGCCTTA ACGAGTACCG GATTTCCTA ATACTCAGCC TACTGCTTAG _n GGCATCCAT	240
CGCAGTT _n GC TATCCACTGG TCCCCCTCGA TTAAACGATT ATAGGTGGTA CAGATATCAA	300
C	301

(2) INFORMATION FOR SEQ ID NO: 4526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4526:

TGATATTATG AGCTGTGTTT TTAGCTTTAG AACCGAAGTC CCCTGCTTTT TTACCAAGAT	60
TTTCAGTAAC TTGT _n CCATC CATTTTTTCT TTTTCGTACC ACCATGGAAT TTTGGCAAAA	120
CACCCATCCG CTGTAACTTC AGAGTGTCAT TGGCATTTAT TACACTATCT CCAACTCCTA	180
GTGGAACAAC CACATCTCGT CTTGGGGTG CATGGAATGT _n CCGTCAGCC CTGTGAATTA	240
T	241

(2) INFORMATION FOR SEQ ID NO: 4527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4527:

CGATCACACT CTTCCGTCGT CATCGCCATT GGCTTTTCAC ACAATACATG GACACCATGG	60
TGTCAATGCT TCTATAGAAA GATCAGCATG GAATTTATTA GGTACAAA TGACCACCGC	120
ATCAACAAGT TTAAACAGCT CGCTAGGTGT CTCAACTGCA TGAGGTATAT TGAAAGCGCT	180
TCGCAACCAT nCAATCATCT GGCACGTGTA TTGAATATCT TGTGACTGGC AACTTAATGA	240
GnACTGTGTC TTTTGAGATT TCCAGnCAAT GCCGGGAATT ATGGACGGGT CTTGGTGGCA	300
ATACCACCCA ACACCT	316

(2) INFORMATION FOR SEQ ID NO: 4528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4528:

GTCCCAAGGG TTGGGCTGTT CGCCATTAA AGCGGTACCG ACGACTGGGT TCAGAACGTC	60
GTGAGACAGT TCGGTCCCTA TCCGTCGTGG GCGTAGAAAT TTGAGAGGAG CTGTCCTTAG	120
TACGAGGAGG AnCGGGATG ACATACCTCT GGTGnACCAG TTGTCGTGCC AACGGCATAG	180
CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAAGCAT CTAAGCATGA AGCCCCCCTC	240
AAGATGAGAT T	251

(2) INFORMATION FOR SEQ ID NO: 4529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4529:

AGTACGTGAC GTTCACTACT CTCACTATGG CCGTATGT CCAATTGAAA CACCTGAGGG	60
ACCAAACATT GGATTGATTA ACTCATTATC AAGTTATGCA CGTGTAATG AATTCCGGCTT	120
TATTGAAACA CCATATCGTA AAGTTGATTT AGGATACACA TGCTATCACT GATCAAATGA	180
CTATTAACAG CTGACGAGAA GATAGCTATG TTGTAGCACA AGCAAACCTCT AATAGATGAA	240
ATGGTCGTT AGGTGATGAG TGTATGCGTT CGGGnACnAT CAGTATGCAA GAAAAGGTTT	300

GTGACGCGAC AGTGTCnA

318

(2) INFORMATION FOR SEQ ID NO: 4530:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4530:

TAGCTGTGTG ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC	60
GGCCTGACAT ACAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGA TCACCAAGTT	120
GAGCAAAGAn GATGTTCTnC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC	180
CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA	240

(2) INFORMATION FOR SEQ ID NO: 4531:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4531:

CGGCTCTTCT GGGACGTAA CCCTAAAGTG CACCCTTCT CCCGAATTAC GGGGTCATTT	60
TGCCGAGTTC CTTAACGAGA TTCGACTCGn TCACCTTAGA ATTCTCATCT TGA CTACCTG	120
TGATCGGTTT GCGGTTAGGG GCACCTATTT TCTATCTAGA GGCTTTTCTC GGCAGTGTGA	180
AATCAACGAC TCGAAGACAC AATGTCTTCT CCCCATCACA GChCAGCCTT AACGAGTACC	240
GGATTTCCT AATA	254

(2) INFORMATION FOR SEQ ID NO: 4532:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4532:

CATTACGTAT AAATGGCAAT CGTGATACTA CAGGTACAAA TGACGCAAAC TGGTCAGCTA	60
TGAATAAACC GAATGTGGCT AAAGTCGTTA ACGCAAATA TGACGTCATC TATAACGGAC	120

ATACTTTTGC AACATCTTTA CCAGCGnAAT TTGTAGTAAA AGATGTGCAA CCAGCGAnAC 180
CAACTGTGAC TGAAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAAC 238

(2) INFORMATION FOR SEQ ID NO: 4533:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4533:

GGTCATTAAT AAAATATCTA AAGCCATTAC TGCATAAAAA TCTCATCAAG CCAATACCTA 60
CATTGTACTA CTGGnCACTT TAGACAGGnC AAGGTGTAG CTACCGATAA TTCAGGAGCA 120
TTAACGCAAC CGACATTTGA CTGTATTAAA TGATAGAGGT TCTGGAAAAC GCCCCAGGTG 180
GTGGAGTTCA AGAAATAATT CACAGGGCTG ACGGAACATT CCTGCACCCC AAGGACGAGA 240
TGTGGTTGTT CCACTAGGAG TTGGAA 266

(2) INFORMATION FOR SEQ ID NO: 4534:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4534:

TACTCAGAGG ATACCCCGAC GTAATGCATT CAATTCAATT TTTAAACGTA TTATTTTCATT 60
GAGCAGAAAG AAAATTATGG CACCAACTT TAATATTTTT TTCAATGTCA TTCTTTTGAn 120
GGGAGTGGGA CAGAAATGAT ATTTTCGCAA AATTTATTTT GTCGTCCCAC CCAACTTGG 180
CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTTTGTnG GGGCCCATCC CCAACTTGCA 240
CATTATTGTA AGCTGACTTT TCGT 264

(2) INFORMATION FOR SEQ ID NO: 4535:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4535:

GCGAATGGAT AACAGTTGAT ATTCCTGTAC CACCTGATAA ATCGTTTTAA TCGATGGGGG 60

GACGCATAGG nATAGGCGAC TGCCGAT E G ATTGCACTCT AAGCAGTAAG GCTGAGTATT	120
AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA	180
GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AAATAGGTGC CCCGTACnGC	240
AAACCGACAC	250

(2) INFORMATION FOR SEQ ID NO: 4536:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4536:

AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC .CAGCTGAGCT	60
AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA TTCGAACCTAC	120
CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC	180
TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAnATAGT AAGTA	235

(2) INFORMATION FOR SEQ ID NO: 4537:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4537:

TGCATCTTCA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT	60
TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT	120
ATAGTTACGG CCGCCGTTTA CTGGGCTTC GATTCGTAGC TTCGCAGAAG CTAACCACTC	180
CTCTTAACCT TCCAGCACCG GGCAGGCGTC AGCCCTATAC ATCACCTTAC GGTT	234

(2) INFORMATION FOR SEQ ID NO: 4538:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4538:

ACCCTCTGCT TGTnAGGCAG ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC	60
CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGACTACC ATCnCGCTA AGGAGCTTAA	120
CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA	180
TGTAATTTAT ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACCATT	240
TA	242

(2) INFORMATION FOR SEQ ID NO: 4539:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4539:

TCATTAACAC CATCACCATA AATAAAACCT TCCATATCTG TTCCTGTGCC AATAAAGCCA	60
TATTGCGTTT GGTCTGTCTG GCCAGTGCAA GATTTCCAAC GATAATTTCT AGGCGTCACT	120
GCTGGCGAAC CATCTAATGG ATAATCATAA TCCATCGTGC GTCCAAGAAG TACTTGTTTT	180
ATTTAAAGTT TGTATTGTGG AATCCTGTGC ACATGTTCTC ACTCCTCTGT ACCT	234

(2) INFORMATION FOR SEQ ID NO: 4540:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4540:

ACACAAAGAA AAATGGCTTG GCGAAGTGAA AACnGTTGAA TCTGACGAAA CGAGAAAAGA	60
GCGCAACGAG TTTAGTAGAG CTAAATGAGT AAGCGAGACC GAAGAGAGGA AAGAAGCnAG	120
CGATTGTCAC AAGTCAAGAA AGGTTCCTAG CGAGGATGGTAGCTAACTTA CGTTCCGCTA	180
GAGTAGAACG TTGCTAGACA AGAAATGAAT GCGATGAGCC GCATTGAGTG TGAAATTGAT	240
AT	242

(2) INFORMATION FOR SEQ ID NO: 4541:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4541:

GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA GTCAAACGCT CACATACGGC	60
TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA	120
ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT	180
GnAGTGTTCT TTCGAACATA GGCGATTATn TCTTATGAAT TCAAGCTTAT TTAAAACTCT	240

(2) INFORMATION FOR SEQ ID NO: 4542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4542:

AAGCTAGCAA TGATGTCAAG CAATGGCAAC ATGTGCTCAn TTAGCTAATA TGCAAGCACA	60
TGGTGAATAT GACGAGGTTG CAACTTCAAC GGCGAGGnTG ATGAATGCCT TACGTTTGCG	120
TGAGACAGTA GCTATGGGCC GCGGTATTAC AGGTGGTAAT GGCATACTGA GCTGACGATT	180
ATGATATTGT CACGTTTTCT TCTCTGTATG CAGAAGGAT TTACACGTAC GAGGTACACA	240
TG	242

(2) INFORMATION FOR SEQ ID NO: 4543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4543:

TGGTGAGCCA TAGAGGATTC GAACCTCTGA CCCTCTGATT AAAAGTCAGA TGCTCTACCA	60
ACTGAGCTAA TGGCTCTTCC ATGGTGCCGG CCAGAGGACT TGAACCCCCA ACCTAGTAT	120
TACAAGTCAG TTGCTCTACC AATTGAGCTA GGCCGGCAAT ATGTAAGATT AAATGGTGGA	180
GAnTGACGGG TTCGAACCGC CGACCCTCTG CTTGTAAGGC AGATGCTCTn CCAGCTGAG	239

(2) INFORMATION FOR SEQ ID NO: 4544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

ATAGAGGATT CGAACCTCTG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC AACTGAGCTA	60
ATGGCTCTTC CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA	120
GTTGCTCTAC CAATTGAGCT AGGCCGGCAA TATGTAAGAA TAAATGGTGG AGAATGACGG	180
GTTCGAACCG nCGACCCTCT GCTTGTAAGG CAGATGCTCT nCCAGCTGAG CTAAATTCT	239

(2) INFORMATION FOR SEQ ID NO: 4545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4545:

AATTCATGCT TTCAAAAGAC GATATACTAC GAACTCCTA CGAACTTGTC CAAGGATTAC	60
GAAAAGACCT AAGGTTATGT AATTGGCCTA AATTTATTAA TCGTTTAAAT TCAGTTAGTA	120
AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAnATA TTATAGAAAA CATCAAAGGA	180
TGTTAAGAAA TACnATTTAT TACCCAGCAT TTAATAATGG TGCTATAGAA GGA	233

(2) INFORMATION FOR SEQ ID NO: 4546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4546:

ACTTTGTTGT CTTCCATCAA CTTGAGACTT CATAACGTTT TGCATCTTCG CCACCTTCAC	60
CACTATTACT CTTTCCACCT AATTGGTTCA TGGCTTGTGC TAnTTTTTCA TGTGCTTCCG	120
CTGAAATCGA TCCATAACTC ATCGCCCCTG TATTAAAGCG TTTGACAATG TCACTTACCG	180
GTTCAACTTG GnCGATGTCA ATCGGTGTAC ATGCTTTAAA TTCAAGTAAA TGTCTAATGT	240
GATCTGT	247

(2) INFORMATION FOR SEQ ID NO: 4547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4547:

GAGGAAATTA CTGAAAACAA TCATCATATT TCTCATTCTG GTTTAGGAAC TGAAAATGGT	60
CACGGTAATT ATGGCGTGAT TGAAGAAATC GAAGAAAATA GCCACGTGGA TATTAAGAGT	120
GAATTAGGTT ACGAAGGTGG CCAAATAGC GGTAATCCAG TGCATTTGAG GAAGACACAG	180
AAGAAGTTTA AACCGAAATA TGnAACCAAG GTGGGCATTA TCGTTGGTTA TCGATTTTCG	240
ATAGTGTACC TCAAATTTCA TGGGTCCAAA TTAATGGTTA ACCCATCCATTGAnGnAGG	300

(2) INFORMATION FOR SEQ ID NO: 4548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4548:

TTGCTATAGT CACCAGACAT ATGAATGTAA ATTATACATT CAAAACTAGA TAGTAAGTCA	60
AAGTGATTTT GCTTCGCAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC	120
AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGGA	180
TCTTGATAAA CCGnAAGTTG GGGAAATCTC ATCTTTACGG GGGGGCTTCA TGCTTAGGAT	240
GGCTTTnCAG CACTTTATGC CCGGTnCCAC ACATTAGGCT TACCCAGCCT ATGCCCCGTTT	300
GGCACG	306

(2) INFORMATION FOR SEQ ID NO: 4549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4549:

ATTTCGATTC GTGATTTTGA ATACTTTTCT TCCACACAAA TGTATACCTA TTGGCATTAG	60
CTTCTACTTT TGTACCATCA ATAAGATTTT GCTTTAAACA TTGACTATGA AACTGGATAA	120
ATAAAGATTC AATTAACGCA TCAGTATTAG GATTCACTCT AATACGATTA ATAGTTTTAT	180
AAGAAGGTGn TTGATTTTGA GCTAACCACA TCATTCGAAT ACTGTATGn AG	232

(2) INFORMATION FOR SEQ ID NO: 4550:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4550:

CTGGGTTTCAG AACGTCGTAT GnAGTTCGGA TCCCTATCCG TCGTGGGCGT AGGAAATTTG	60
AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG TACCAGTTGT	120
CGTGCCAAng CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AACATTCTTA	180
AGCATGAAGC CCCCCTCAAG ATGAGATTTT CCAACTTCGG TTATAAGATC CCTCAAAGAT	240
GATGAAGTTA ATAAGTTC	258

(2) INFORMATION FOR SEQ ID NO: 4551:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4551:

TTACAGGCAT GCGAGTTGGG GTGAGGGCCC ACACAGAAGC TGACGAAAAG TCATGACAAT	60
AATGTGCAAG TTGGGGATGG GCCCACAAAG AGAAATTGGA TTCCCAATTT TACAGACAAT	120
GCAAGTTGGG TGGGACGACG AAATAAATTT GCGAAAATAT CATTTCTGTn CCCTCCCTCA	180
AAAGATGACA TTGAAAAAAT ATTAAAGTTG GTGCCATATT TTCTTCTGCT CATGAATATA	240
CGTTAAATTT GATTGATCAT CGCGAATTGA TATTATTCTC ATATAAAAA TACTTATTAC	300
ACTTACCGTA TGATAGTTTG nTATATACTC TGATAAAGTC AAACCTAATA GCGTTTCTAG	360
CTGTGnGTGT TTCATAATTA TATACATTAT CAGGCTTTAA	400

(2) INFORMATION FOR SEQ ID NO: 4552:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

ATAGGAAACT GCCAATTGGA CGGTTGCCGC ATTCAAACCC AGCACGATTA CGGCGAATTG	60
CACGTGAAnC ATTTCTACAG CTTGATCTTG ACCTATGATT TTAATTCTTA AACGATTAGA	120

AATATTTTTT AAACGTTCAA TATCGTTATC ATCCATTTGG AGAAACTGGG AATACCATTG	180
AATCGTTGnA ATAGTATCTG GAAATATCAT GGAAGTGTAG CAACAGCAGT GTGTTGCACC	240
ATTnACTGAT TTTGCTAATT TATCTTGGTG AATGGATTTG GATTTGCATT TTGGAATGTG	300
CGTGCAGCTT TT	312

(2) INFORMATION FOR SEQ ID NO: 4553:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4553:

AGCAGCGATC AAAAATAATC CGCAATACGC TGGCAAATA CCAATACCAA ACCATAGAAC	60
AACAAATGGT GCCCATGCTA TCGGAGATAT CGGCCTAAT AATTGAAATA GCGGTTTCGAT	120
AGCGTTGTAT AGCCAACGAT TCCTTCCAAG CAAGAAGCCC AATGGAATAG CAACCAACAA	180
TGCGACAACA AAGnCCGCTA CAAATCTCCA TGAATAATT GCTAAATGTG GnGAATTTCT	240
CCAGTAACAA TGGA	254

(2) INFORMATION FOR SEQ ID NO: 4554:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 4554:

GGTCTGAATC GCTATCTGAG TCTGAATCGC TATCTGAGTC TGAATCACTG TCTGAGTCCn	60
AGTCACTGTC TGAATCTGAC TCACTATCTG ATTCTGAGTC GCTATCTGAT TCTGAGTCGC	120
TGTCTGGAAT CTGAATCACT GTCTGGAATC CGAATCGCTA TCTGGATCTG AGTCGCTATC	180
TGAACCCGAG TCGCTGTCTG AGCCTGAGTC ACTGTCTGAA ATCGAAATCG GAACCCGGGn	240
CTGGGGCTTG G	251

(2) INFORMATION FOR SEQ ID NO: 4555:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4555:

TACACAAAGA GATAAATTAC TTATGCAAAG GCGGAGGAAT CACATGTCTA TTACTGAAAA	60
ACAACGTCAG CAACAAGCTG AATTACATAA AAAATATGG TCGATTGCGA ATGATTTAAG	120
AGGGAACATG GATGCGAGTG AATTCCGTAA TTACATTTTA GGCTTGATTT CTATCGCTTC	180
CTATCTGAAA AAGCCCAACC AGAATATGCA GTGCCCTGTC AAGnGAAGAC ATCACGTTC	240
AGAAGCATGG C	251

(2) INFORMATION FOR SEQ ID NO: 4556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4556:

AGCTACCCCG GGGATAACAG GCTTATCTCC CCCAAGAnTT CGCATCGACG GGGAGGTTTG	60
GCACCTCGAT GTCGGCTCAT CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT	120
TCGCCCATTA AAGCGGTACG GAGGCTGGGT TCCGAACGTC GTGAGnCCGT TCGGTCCCTA	180
TCCGTCGTGG GCGTAGGAAT TTGAGAGGAG CTGTCCTTAG TACGAGAGGA CCGGGTGGAC	240
ATA	243

(2) INFORMATION FOR SEQ ID NO: 4557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4557:

TAACTTAATC TATGTTTCCA CCATTTTTAT AAGTCAAACG CTCnGGGGGG GGCTTCGTTT	60
TCATTATTTT AAATGCTCAT TTACATAAGT AACTCTGCT TAAAATAAT TAACTCATT	120
GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG TTATTAATCT TGTGAGTGTT	180
CTTTCGAACA CTAGnCGATT ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTG	235

(2) INFORMATION FOR SEQ ID NO: 4558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4558:

CCGTTAAGCA CTAAATCCGC TTAATAACGG CTTTCTATCG CGCGCAACAT TCGTTTGAC	60
TGCTTTTTTCT TTCAAAGCTT GACGTTATCA TATTTTTTCT TACCTCGTGC ACACCAAGTA	120
ATACTTTACA ATGTCCATGC TTCAAATAAA GCTTTAACGG ACAATCGAAT AACCAAnCTC	180
ACGTGTTTGA TCACCCAATT TAATGATTTC ACGCTTGTGC AATAATnATT TTCGAGACGA	240
GAGGATCGGA TTAACGAT CCCCTCCTCG TATGG	275

(2) INFORMATION FOR SEQ ID NO: 4559:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4559:

TTATATGGAT GTATCGCCGA AGCAAGTTGT TTCAGCAGCG ACAnATGTAT TCCGATGACT	60
CAAACCGTGC ATTGATGGGT GCGAACATGC AACGTCAAGC AGTGCCTTTG GATGAATCCA	120
GAAGCACCAT TTGTTGGTAC AGGTATGAA CACGTGCAG CACGTGTATT CTGnGTGCGG	180
CTATTACAGC TAAAGCACAG AGGTCGTGTT GAACATGTTG GAATCTAATG AAAT	234

(2) INFORMATION FOR SEQ ID NO: 4560:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4560:

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG	60
TTCTACTCTA GCGGAAnTAA nTGGCTACCA TCGTCGCTAA AGACCTTtT TGA CTGTGTGA	120
CAATCGCTTG CTTCTTTCCT CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTA CTAACT	180
CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AG	232

(2) INFORMATION FOR SEQ ID NO: 4561:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4561:

TCAAAGGACG CATACCATTA CGGGTCTGCT ACTTGTAAGC ACACGGTTTC AGGTTCTATT	60
TCACTCCCCT TCCGGGGTGC TTTThACCTT TCCCTCACGG TACTGGTTCA CTATCGGTCA	120
CTAGAGAGTA TTTAGCCTTA GGAGATGGTC CTCCCAGATT CCGACGGAAT TTCACGTGCT	180
CCGTCGTA CT CAGGATCCAn TCAAGAGAGA CAACATTTTC GACTACAGGA TTATTACCTT	240
CTTTGATTCA TCTTGTC	257

(2) INFORMATION FOR SEQ ID NO: 4562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4562:

TACCTAATAA GTTGTGAATT TGAACAGCGG CTGCTTTACA nTGGAAGTGC TGATTCAGTT	60
GCCACAATTA CCATACCAAT TTTCTTTTTG TCTTCGCTCG ThATAATGTC CTTAGCAGCG	120
TTAGCTCCGA TTGAAACGAT GTCTTGTTT ACAGGACTAA CAGCATTTT AGTTTGACCA	180
ATTCCAATTA AAAATTTGTT TGGGTCTACT TGGCGTGGCT TCCTGCTGAA TTTAGCCATG	240

(2) INFORMATION FOR SEQ ID NO: 4563:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4563:

CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC	60
TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACCTAAT CTATGTTTCC ACCATTTTTTA	120
TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTATTTT AnATGCTCAT TTACATAAGT	180
nGACTCTGCT TTAAAATAAT TTAACCTATT GTCTGCTAAA CGTTT	225

(2) INFORMATION FOR SEQ ID NO: 4564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4564:

TGTTAATTGG nGAATTTGGA TACTGGTTAT ATTCAGCTGC ACCGCAAGCA ACTTCTATTG	60
ATGGCCTAAC TGCCTTTTTA CCTCAAGCAA TGGGTATGGT AATTGTTGCA GTCATTTATG	120
GCTTTATGAA TATGAAAGCA GAGGAATCCC ATTCCCGTAA TAAAATTACG GTGGTTACAA	180
AATTATTTCA GGTTTCTTTC TTTTGCATTT GGGTGCTTTA ACCATATCTT nTT	233

(2) INFORMATION FOR SEQ ID NO: 4565:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4565:

AGCTCAGATA GCGCTCAGAC TCAGACAGCG ACTCAGATTC AGATAGCGAT TCAGACTCAG	60
ACAGCGACTC AGACTCAGAC AGCGACTCAG ACTCAGATAG CGACTCAGAT TCAGATAGCG	120
ATTCAGACTC AGACAGCGAC TCAGATTCAG ATnGCGATTC GGAnTCAGAC AGCGATTCAG	180
ATTCAGACAG CGACTCAGAC TCGGATAGCG ATTCAGATTC AGATA	225

(2) INFORMATION FOR SEQ ID NO: 4566:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4566:

CCAACTGGAG CTAATGGCTC TTCCATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC	60
TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG	120
TGGAGAnTGA CGGGTTCGAA CCGCCGAnCC TCTGCTTGTG AAGGCAGATG CTCTCCCAGC	180
TGAGCTAATT CTCCGATTTA AAACTGGCCT GGGCAACGTT CTA CTCTAGC GGGAAC	237

(2) INFORMATION FOR SEQ ID NO: 4567:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4567:

GTTGGAGATA GTGTAATAAT GCCAATGAGC CACTCTGAAG TTACAGCGGA TGGGTGTTTT	60
GCCAAAATTC CATGGTGGTA CGAAAAAGAA AAAATGGATG GAAACAAGTT ACTGAAAATC	120
TTGGTAAAAA AGCAGGGGAC TTCGGTTCTA AGCTAAAAC ACAGCTCATA ATATCAAAAA	180
GGTGCAGAGG AAATGGTTGA nnGGCAGCGG ATAAATCAAG ATGGTGCAC TGGTTAGCGT	240
TAAATCGCGA TGTGTGGGTT AnTACACATC CGGGAAGTAG TAATAAGTAT GTCAGTTTAA	300

(2) INFORMATION FOR SEQ ID NO: 4568:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4568:

ATCCCGTGGA GGTTCAAGTC CTCTCGGCCG CATCAAAATT CTTAATTTAA AAAGCGGGT	60
GTAGTTTAAT GGCAAAACCT CAGCCTTCCA AGCTGATGTT GTGGGTTCGA TTCCCATCAC	120
CCGCTCCATA GATAATTTTA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT	180
TCCAAAAACG TAACTATAAG TTACAAACAT TnATTTTAGT ATTTGATGGA GCCTnAATCC	240
AAACATTCCA	250

(2) INFORMATION FOR SEQ ID NO: 4569:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4569:

GATCCCCTAG CTTTACGTTC AACTTTATAT GGGTATAACT CGAATATAAT TTGGCGCTCT	60
ATGTCATGGG ACAACGAGTA GACATTTAAT AACGGATCAG GTTCTGGTGA CGGTATCGAT	120
AAACCAGTTG TTCCTGAACA ACCTGGTAg CCTGGTGAAA TTGAACCAAT TCCAGAGGnT	180
TCAGATTCTG ACCCAGGTTC AGATTCTGGG CAGCGnTTCT AATTCAGATA GCGGT	235

(2) INFORMATION FOR SEQ ID NO: 4570:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4570:

AATCTATTTT	TTCTATTGTT	AAATCGCTAT	CTCCATCTTC	TTTATCTCT	GGTATTATTT	60
TTTCTTCAAC	TAAGTCACGA	TATAATGTTT	TTGAATTTTC	GTTCAATTC	GATTCGTGAT	120
TTTGAATACT	TTTCTTCCAC	ACAAATGTAT	ACCTATTGGC	ATTAGCnTCT	ACTTTTGTAC	180
CAnCAATAAG	ATTTTGCTTT	AAACATTGAC	TATGAAACTG	GGA		223

(2) INFORMATION FOR SEQ ID NO: 4571:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4571:

CATGATATTT	TGAACCGCAT	GGTTAAAGTT	GCAAAGACGG	TCTTGCTGTC	ACTTATAGAT	60
GGATCCGCGC	TGCATTAGCT	AGTTCGTAAG	GTAACGGCTT	ACCAAGGCAA	CGATGCATAG	120
CCGACCTTAG	AGGGTGATCG	GCCACACTGG	nACTAAGACA	CGGTCCAGAC	TCCTACGGGA	180
GGCAGCAGTA	GGGAATTTTC	CGCAATGGGC	GAAAGCTGTA	CGGCGCAACG	TCGTGTGnAG	240
TGCTGCAGGT	TCTTCGGATC	GTAAAT				267

(2) INFORMATION FOR SEQ ID NO: 4572:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4572:

AATnCAACTT	TTACTTACTA	TCTAGTTTTG	AATGTATAAA	TTACATTCAT	ATGTCTGGTG	60
ACTATAGCAA	GGnGGTCACA	CCTGTTCCCA	TGCCGAACAC	AGAAGTTAAG	CTCCTTAGCG	120
TCGATGGTAG	TCGAACTTAC	GTTCCGCTAG	AGTAGAACGT	TGCnGGCAT	AATATTAATC	180
CACAGTAGCT	CAGTGGTAGA	GCTATCGGCT	GTTAACCGAT	C		221

(2) INFORMATION FOR SEQ ID NO: 4573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4573:

```
GCAGAAATGC CAGCCGCATT GAGTGAACAC AGAGTTACAG GGTATTCTGT AGCCGAACCA      60
TTCGGTGCAn TGGGGGAAAA GTTAGGCAAA GGTAAGACTT TGAAACATGG TGATGACGTT      120
ATACCTGATG CGTATTGCTG TGTGCTAGTA CTnAGAGGGG AATTGCTTGA TCAACACAAG      180
GATGTAGCGC AAGATTTGTA CAAGGTTATA AAAAGTCTGG CTTTAAAATG      230
```

(2) INFORMATION FOR SEQ ID NO: 4574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4574:

```
TCACATATCG ATAACATGAC ATAACTCATG CTGGGTTTCC CCATTCGGAA ATCTCTGGAT      60
CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC      120
TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAnACTTAAT CnATGTTTCC ACCATTTTTTA      180
TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTAnTTT AAATGGCTCA      230
```

(2) INFORMATION FOR SEQ ID NO: 4575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4575:

```
CTTACAATAG TGTGCAAGTT GGGGTGGAGC CCCGnACAG AGAAATTAGC TCCTCAATTT      60
CTACAGACAA TGCAAGTTGG CGGGGCCCCA ACACAGAAGC TGGCGAAAAG TCAGCTTACA      120
ATAGTGTGCA AGTTGGGGTG GGACGACGAA ATAAATTTTG CGAAAATATC ATTTCTGTCC      180
CACTCCCAAA AAGACCGCAG TAGGATAATT CCATTTGGAA ATACCTTACT GCCnGTTTTT      240
AAAGTAATAG CnAATATTTT GGAATTAnGT TTCCTAGTTA ACCATACCAA CTAATGGCCT      300
```

CCTTAAATT

309

(2) INFORMATION FOR SEQ ID NO: 4576:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4576:

TGATTCTAGG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGGTAAA	60
ATCTATATTT TACTTACTTA TCTAGTTTTT AATGTACAAA TAATGGTGGG CCTAAGTGGA	120
CTCGAACCAC CGACCTCACG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC	180
ATTTTTTTGA ATGTTAAATA AACATCnAAA CTGGnATACC ATATGTCACG GTAATCCGCA	240

(2) INFORMATION FOR SEQ ID NO: 4577:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4577:

CTTCGTGTTA AAATTTGATG CACAATGGTC ACATTTTTTA TCTTTCCAAT AAGTACTGTC	60
TGGGTAAAAA TnTATTAATT GGGTGGTTCG TGAAATGCAA TCTTTTTAAC GACTTCAGGG	120
TAATCTTTTA ACACATGCAT CGCAACGATT GAACCTnAAC TTGAACCTAA TATATAGACA	180
GGTTCATCAC TTAATGACTT TGCAAGTTCG GCAATGTCCT GTGCGTCGCG TTT	233

(2) INFORMATION FOR SEQ ID NO: 4578:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4578:

TAGGCATACC AAAGTCGATA CCATAGTGAC GACCGCCATT AAAGTTAAGT CCACCTGTGT	60
AACTCCCAA CCTTTGCCAA ATTGGATGGT CAAATAGATA GCTTCCATCG CCTCCGCCAC	120
CAAAATCTTC AAACCACGAT TTACTTTGnC TACTAATTTC TTTTGTAGCA ATGAGTACGC	180

GCCTTAGCAA TTTTAnGTAG CGTAGTCCGC TCCAAAATAA TATTAACTG ACATACTTAT	240
TACnAGTTCC CTGGATGTGT ACATAATCCA CACATCGCGA TTTATCGCTA ACAGAGCACA	300
CTTGATTACG CGCGCTCAAC ATTC	324

(2) INFORMATION FOR SEQ ID NO: 4579:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4579:

AATGTAAAAA CTGATTTCTA TTAATTATTT GATAGAAATC ACTTTTTTGT ATTTTATAAT	60
GTACAGCTCG TTGCATTCAT ATAGCTTGAA GTCACGTTTA AAACCATATC TATCATTATG	120
GTATGCATAT CGTTTAAAC CTATTCTTTT GTTAnTAGGA CATATAAATT CATCATTAAT	180
TCGTCATATT TCCAATTTTG AGTGThAAAA ATGTCACTTT TAAACTTTC	229

(2) INFORMATION FOR SEQ ID NO: 4580:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4580:

CGGGGACTCn AACCCGTGTT GACCGCCGTG GAAAGGGCGG TGTCTTAACC GCTTGnACCA	60
AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG	120
CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA	180
CGTAAGTTCG ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCGGC ATGGGAACA	239

(2) INFORMATION FOR SEQ ID NO: 4581:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4581:

CCGnACGAAT TTACACGTGT TCCGTCGTAC TCAGGATCCA CTCAAGAGAG ACAACATTTT	60
CGACTACAGG ATTATTACCT TCTTTGATTC ATCTTTCCAG ATGATTCGTC TAATGTCGTC	120

CTTTGTA ACT CCGTATAGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT GTnTTGGGCT 180

CTTCCCGTTT CGCTCGCCGC TACTAAGGGA ATCGAATTTT CTTTCTCTTC CTC 233

(2) INFORMATION FOR SEQ ID NO: 4582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4582:

TTAGTAAAAA GTCTGTGAGT AAGGGTGTAT GGAAAGTGGT TAAATATTAT AGAAAACATC 60

AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTTAA TAAEGTGCT ATAGAAGGAA 120

TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTTGG TTACAGAAAT TTCAnCAnCT 180

TTAAAGCACG TATAATGATG GATTTTCAGC TTGTACAA 218

(2) INFORMATION FOR SEQ ID NO: 4583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4583:

TAATAAACAT GCCATACGTA ATAAGTGGCG TTGTATTAAA ATCATCTATA ATAGCCATAT 60

AGTTTTGCTC ACTACCATAA CCTGCATCAG CTACAATATA CTCCGGTAAA TAACCGATGG 120

ATTTTGGAAT CATTGTTAAA AATGGAATTA AAGTTCTAGT GATCTGTTGG GTTTTGGAAA 180

TAGGTCATAG GGtnAAAACn TTTTGTAGAA TTTGTGCTA TTTGTAAAT TGTATCCCGG 240

CTTGAAGTTG G 251

(2) INFORMATION FOR SEQ ID NO: 4584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4584:

TTTAGGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTCGTA GCTTCGCAGA 60

nTAACCCACT CCTCTTAACC TTCCAGCACC GGGGCAGGCG TCACCCCTAT ACATCACCTT 120
 ACGGTTAGCA GAGACTGTGT TTTTGATAAA CAGTCGCTnGGCCTATTCAA TGGGGGCTCT 180
 TCTGGGGGTT AAACCTAAAG AGCAACCCTT CTCCCGAAGT TACGGGGTC 229

(2) INFORMATION FOR SEQ ID NO: 4585:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4585:

TTATAAAAAG ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ATAGCGATTA 60
 TTTCTTATGA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGC TTGGTAAAT 120
 CTATATTTAC TTACTTATCT AGTTTTCAAT GTACAATTnC TTTTtagTCA AGCGCTCGCA 180
 TACTGCTnTA TTTTCAAAAA ATCAAATGCT CATTTACA 218

(2) INFORMATION FOR SEQ ID NO: 4586:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4586:

GGGGGGGGGC CTTGCCACT GGTGTTCTC CATATCTCTG CGCATTTTAC CGCTACACAT 60
 GGAATTCCAC TTTCTCTTC TGCACTCAAG TTTTCCAGTT TCCAATGACC CTCCACGGTT 120
 GAnCCGGGGC TTTTACATC AGACTTAAAA AACCGCCTAC GCGCGCTTGT ACGCCCAATA 180
 ATTCCGGATA ACGCTTGCCA CCTACGTATT TACCGCGGGC TGCTGGCACG TATTnAGCCG 240
 T 241

(2) INFORMATION FOR SEQ ID NO: 4587:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4587:

CAGCCACCTG TTGCCACCAG CTACACTTGC ATTGTTTGCT ACGACACGCC CAAACAATGC 60

TGAAGTGAAT AAGAAATCAA TCATTTGCTC TTCTGTTAAA TCATGTGTTT TTTCTAATTT	120
AAAAAGTGCA CCGGGAATGG TACCCGAGGA ACCAGCTGTT GCGGTTGCAC AAATAAACC	180
CATCGCAGCA TTGACTTCAT TGTGCAAGG CACnTTGAC TCGGCAATC ATTCATATCC	240
GACnAAGCAG ATG	253

(2) INFORMATION FOR SEQ ID NO: 4588:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4588:

ATGAACGGGT GGTAGCGAGT GGACGAAAAA CATCAATGAA AAGCTAGCTG TAGTTGCAAG	60
AGAAACTGGC TTACGATGGC ATTGGATCAA CACATGCGGC ATTGAGAAAT CCACGCATGG	120
CTGAGACGTT TACGATTGCG CGAAAAATGA ATCCTGAAGG CATTTTAGCA ATGTTGGTGC	180
GGACGTACCA GTAGAAAAGG CTTTGGAAGC AGTTGAAT	218

(2) INFORMATION FOR SEQ ID NO: 4589:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4589:

GCCATGGCTC CACAGGTAGG ACTCGAACT ACGACCGATC GGTTAACAGC CGATAGCTCT	60
ACCACTGAGC TACTGTGGAT TAATATTATG CCTGGCAACG TTCTACTCTA nCGGAACGTA	120
AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT	180
GACCTCCTTG CTATAGTCAC CAGACATATG nATGTA	216

(2) INFORMATION FOR SEQ ID NO: 4590:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 234 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4590:

AGATTTAAAT AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC	60
ATCnCATTCa TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT	120
CCTCGGCTAA GAACCTTTCT TGACTTGTGA CAATCGGCTT GCTTCTTTCC TCTCCTTCGG	180
CTCTCGCTAC TCAATTTAGC TCTACTAAAC TCGGTTGCGG CTCTTTTCTn GTTT	234

(2) INFORMATION FOR SEQ ID NO: 4591:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4591:

AATTGACTGA CTTCGTTTTA CCGCGTGTTT AATATTGTTA TACATATATT CTAATTGCAC	60
ATTTAAACTT CGTAAATGCC AATGTGnGTG GGACAGAAAT GATATTTTCG CAAAATTTAT	120
TTCGTCGTCC CACCCCAACT TGnACATTA TTGTAACCTG ACTTTCCGCC AGCTTCTATG	180
TTGGGGCCCC GCCAACTTGC ACATTATTGT AAGCTG	216

(2) INFORMATION FOR SEQ ID NO: 4592:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4592:

ATTCCGGATA ACGCTTGCCA CCTACGTATT ACCGCGGCTG CTGGCACGTn TTAGCCGTGG	60
CTTTCTGATT AGGTACCGTC AAGATGTGCA CAGTTACTTA CACnATGTT CTTCCCTAAT	120
AACAGAGTTT TACGATCCGA AGACCTTCAT CACTCACGCG GCGnTGCTCC GTCAGGCTTT	180
CGCCATTGCG GAAGATTCCC TACTGCTGCC TCCCCG	216

(2) INFORMATION FOR SEQ ID NO: 4593:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4593:

TTGGACTAGA ACCAATGAAG GACGTTACTA ACGACGATAT GCTTAAAGGA GCTGTAAGTA	60
---	----

AGCTTTGATC CAGAGATTTTC CGAATGGGGA AACCCAGCAT GAGTTATGTC ATGTTATCGA	120
TATGTGAATA CATAGCATAT CAGAnGGCAC ACCCGGAGAA CTGAAACATC TTAGTACCCn	180
GTGGAAGAGA AAGAAAATTC GATTCCTTA GTAGCGGCGA GCAGAACG	228

(2) INFORMATION FOR SEQ ID NO: 4594:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4594:

CAATCGTTGA AGGAAATGTA CCAGCAGCAA TCAAAGACAA AGAAATTATT TCTGTAGACA	60
TTTCATCATT AGAAGCTGGA ACGCAATATC GTGGTGCTTT TGAAGAAAAT ATTCAAAAAT	120
TAATCGAAGG TGTTAAATCT TCACAAAATG CCGTACTATT CTTTGATGAA ATCCATCAAA	180
TTATCGGTTT AGGTGCCACA GnAAGTGGAT TCCAGGTTAGCCAAAGGGGT TAATCTGGAT	240
TAATTTTTTTT Tn	252

(2) INFORMATION FOR SEQ ID NO: 4595:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4595:

ACTCTCTAGT GACCGATAGT GAACCAGTAC CGTGAGGAGA AGGTGAAAAG CACCCCGGAA	60
GGAGnTGAAA TAGAACCTGA AACCGTGTGC TTACAAGTAG TCAGAGCCCG TTAATGGGTG	120
ATGGCGTGCC TTTTGTAGAA TGAACCGGCG AGTTACGATT TGATGCAAGG TTAAGCAGTA	180
AATGTGGAGC CGTAGCAGAA GCACGGTTCT GGAATAGGGG CGTTTTAGTT ATTTTGGGTC	240
GTTACCCGGG AGnAAAGG	258

(2) INFORMATION FOR SEQ ID NO: 4596:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4596:

CCTACCGCTG CAGCCGCTGG ATCTGCTGGA GTTGCATTAG GATCTGCCGG TGCCGCACGT 60
CTACTTCTCT TTTTCGGTCT ATTAGATGCT GGTTCAGCAA TTGCAACTAG CTCTGGTTTA 120
TTTGAAGAAT GACGAACATC TTCTTGAATT TCCTTTAAAG TAGATGTCCT CCTGAACCAT 180
TnCATTTGTTT AGTTGGGTAC ATTAATGChG TATTATGAC ACTACATCA 229

(2) INFORMATION FOR SEQ ID NO: 4597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4597:

GCTCACCTTA GAATTCTCAT CTTGCACTCA CCTGGTGGTC GGTTTGGCGG GTAGGGTCAC 60
CTATTTTCTA TCTAGCAGGC TTTTCTCGGC AGTGTGAAAT CAACGACTCG AAGnCACAAAT 120
GGTCTTCTCC CCATCACAGC TCAGCCTTAA CGAGTACCGG ATTTGCCTAA TACTCAGCT 180
TACTGCTTAG ACGTGCAATC CAATCGCACG CTTCGCCTAT CCTACTGnGG TCCCCCATC 240
GATTAA 246

(2) INFORMATION FOR SEQ ID NO: 4598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4598:

AAGAAAATAA AGAATGCTAC AATTACGATT GCAATCAAAC CAAAGAACCA TAATGATGTG 60
TACCAAGTGC TGCACCTTTA GTAATGACAA CGTTTAAACT TAGCAACATA ACTACTAGAA 120
CAATTAGCCC TGCAACGTCA AATTTATGTG TATTGGTAAT TTCTGATTTT GTTTCAGGCG 180
TCCCTTTGAT GAGTAGCATT GAAAGTACGG nAACGATGnG TTG 223

(2) INFORMATION FOR SEQ ID NO: 4599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4599:

nTnTCACTGT TTGACCCGGT ACCGTGTAG ATAATCCCGC ACGCAATGCA ATCGTTCGTG	60
CAATGTTTTG GCCTTGTAAT CCTTCTGGAA AAGCCGTACC AACAATGACA TCTTCAATCA	120
TATTCTTATT GAATTTTCCG TCAATACGTT TCAATACGCC TTGTAATACT TTGGCTGCGA	180
CATCATCAGG TCTTTCGTGG AATAATGCGC CTGCTTTGC	219

(2) INFORMATION FOR SEQ ID NO: 4600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4600:

AAGGTTAAGA GGAGTGGTTA GCTTCTGCGA ATACCGAATC GAAkCCCCAG TAAACGGCGG	60
CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC CGACCCGCAC	120
GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACGAGAGACT CGGTGAAAAT CATAGTACCT	180
GTGAAGATGC AGGTTACCCG CGGACAGG	208

(2) INFORMATION FOR SEQ ID NO: 4601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:

AGTGCCAGTG ATTAAGTCA TTTTCAATA GATCAGGGAA GACTACCAAG CTTATGTTGA	60
AGGACATCTT TTGGCGTTAC CGGTTGGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT	120
CACTTGAACA ACATTTGTTA ACGATTATT TGGCAATTCG TTATTGTCTGA ACAnTGcNAG	180
TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG	240
TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAC TACAAC	286

(2) INFORMATION FOR SEQ ID NO: 4602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:

ATATGGCTAT GGTATTACACA TATCGATnAA CATGGACATA ACTATGCTG GGTTTCCCCA	60
TTCGGGAAAT CTCTGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT	120
AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA	180
TGGTTCCACC CATTTTTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG	240
nTTAAACGGG GTATTAATCT TGTG	264

(2) INFORMATION FOR SEQ ID NO: 4603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:

GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAAGA GTAATAGTGG TGAAGGTGGC	60
GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAAAGTAA GTGCGATTAA	120
ACAAGTTGCT TCTGGGCGTT TTGGTGTAnC TAGTGATTAT TTACAACATG CCAAAGAATT	180
CAAATTAAAG TTCGCCAGGT GCAAGCCCTG GTGAGGTGGT CATTACCTGG TACTAAGGGA	240
TATCCn	246

(2) INFORMATION FOR SEQ ID NO: 4604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:

ATTAAC TAAC ATGGGCATCT ACGATGGAAA CAGACGTGGTATCCTCGCTA TTATCCAGCT	60
AnCGCCATGC TGGCTCGTTT TTCAAATCAA GCCATTTTAA ATTTTGGAAA GGTGTATGGA	120
CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATCGCCAT GTCTCATGGA	180
GAAAATCAAG AGCATCATTC AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn	240
TTTGATGG	248

(2) INFORMATION FOR SEQ ID NO: 4605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:

```
CAAGTTTTC AGTTTCCAAT GACCCTCCAC GGTTGAGCCG GGACTTnTCA CATCAGACTT      60
AAAAAACCGC CTACGCGCGC TTTACGCCCA ATAATTCCGG ATAACGCTTG CCACCTACGT      120
ATTACCGCGG CTGCTGCAC GTATTAGCCG TGGCTTTCTG ATTAGGTACC GTCAAGATGT      180
GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTTG TTTTGTnTTTn      240
TGGGTT                                         246
```

(2) INFORMATION FOR SEQ ID NO: 4606:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:

```
CTTCTTACCA GTCGTTGTAC CTGTGCGATT CAATTGTGC ACTGCTTGCT CTAAGGCATG      60
TGTATCTGCA GTTAAATCAT GTnTCGCTTG GTTTAATGCT GTTAATGCGT TATCGACACG      120
ATGTTTTTCA TCTGAAATTT GTTGTGCAGT TGCATCGCCA TTGTCAATAA CACGTTGAGC      180
TGCAGTTATT TCAGTTTCTG CTTCACGCTn CT                                         212
```

(2) INFORMATION FOR SEQ ID NO: 4607:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:

```
TAGTCAAGAT GAGAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAAT      60
GACCCCGTAA CTTCTGGGAGA GGGGTGCTCT TTAGGGTTAA CGCCAGAAG AGCCGCATGA      120
ATAGGCCCAA GCGACTGTTT ATCAAAAACA CAGGTCTCTG CTAAACCGTA AGGAnTGTAT      180
AGGGGCTGAC GCCTGCCCGG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC      240
GGAATCGAAG CCCAGTAAA CGGCGG                                         266
```

(2) INFORMATION FOR SEQ ID NO: 4608:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:

```
TTCAGTACGT AAATACGCAC GTGAAAAAGG TGTTAnATTA AAGCAGTTTC TGGATCTGGT      60
AAAAATGGTC GTATTACAAA AGAAGATGTA GATCATACT TAAATGGTGG TGCACCAACA      120
GCTTCAAATG AATCAGCTGC TTCACTGACA AGTGAAGAAG TTGCTGAAAC TCCTGCAGCA      180
CCTGCAnCAG TGAACATTAG AAGGCGACTT CCCAG      215
```

(2) INFORMATION FOR SEQ ID NO: 4609:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4609:

```
GGGTTCATAC ATGTCAATAG TAACCGTCTT AACTTGTTGT CGATTTTTTA AATGAATCG      60
CTCGAAATAG GCACGCAAGA ATCTTGTAGT TCTATTTTCT AAAATATCTA TAACATCATG      120
GTATCATTAT CTATAAAAT GAAACTCATT GATCCAGTTA CATTTTAAAC GCTTTTAAAT      180
TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATTChGA ATnGATTAGC      240
C      241
```

(2) INFORMATION FOR SEQ ID NO: 4610:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:

```
ATTCATTTCT TGTCTAGCAA CGTTCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG      60
CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC      120
TTRACTATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG      180
TTTCAnTTCG CCAAGCCATT TTTCTTTGGT GnTTA      215
```

(2) INFORMATION FOR SEQ ID NO: 4611:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:

GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAGC TTCATGCACA	60
TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTGTGATA AATATGGCGTGCGTTTGGCA	120
ATAGCATTAA TGCGCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA	180
TGCAGTACCG TGTTTGTGTA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT	240
TAAATTATCT TGTGATTCAG GTAAATCCAT CTTGTAGCT ACTACGATTT GAGGTCTATC	300
TTCTAAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTTATAA TCTTCAATAG	360
GGTCTCTACC TTCAGAACCG CTCCATATCC ATCCTGTGGA	400

(2) INFORMATION FOR SEQ ID NO: 4612:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:

AATACTATTA AGAAGTCCTG AAAAATTCAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA	60
TGATAAGTAT GCAAATAATT TCACAGTGT TGCAGCAGGG GCAATTATGA TTGCAGTACC	120
TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTTAGTA TCAGGTTTAA CAACAGGTGC	180
CGACCAAAGG GTTAGTTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCTAATG	240
ACCGTTAAGG TTnAAAGG	258

(2) INFORMATION FOR SEQ ID NO: 4613:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:

GACTTCGTTT CAGTGTA AAA TTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG	60
ATTAGTGCTT CATCTTTTTT ACCCCAATAT TTTATAAGTG CAATTCGTAT GTGCACGTGC	120
TTTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC	180
AGCTTTTTTC TACAGCTTTT ACAATATTnn	210

(2) INFORMATION FOR SEQ ID NO: 4614:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:

TAGCGTATTA ATCGGCGGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG	60
AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGnATCGCT	120
ATCTGAATCT GAATCGCTAT CGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA	180
GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA	235

(2) INFORMATION FOR SEQ ID NO: 4615:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:

ATGTGCGTGG TTTATTTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTTAA nTTTA	60
TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTTCG AECTTTAAT TCAGTTAGAA	120
GCATCATAGA ATGCATGATT ACTGTTGTAA AGATACGTAA TGTTTTGTAT TGACTGTATG	180
TCnTTGGATA GAGTTACAAA CTTATTTTG	209

(2) INFORMATION FOR SEQ ID NO: 4616:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:

ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA	60
---	----

TGTGCGAnAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT	120
GAGTGCTAAG TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGCTAACGCA TTAAGCACTC	180
CGCCTGGGGA GTACGACCGC AAGTTGGAAA CTCAAAGGAA TT	222

(2) INFORMATION FOR SEQ ID NO: 4617:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:

CAGTTTGCAA CAÖCCAATT CTTGCCAGTC AGCATGATTC TGTTCATTTT TGCGATTTCT	60
TTGTCGATAT TTTCAAATCT TGTTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA	120
ATGTATCAAC ATATCGCGGT ATGTTTAAGT TGTAATCGTT ATCGGnGATC TCTTGTAATG	180
TCGCGCTGTG GCTATATTTA TCAATCGTGG CTTTACGCT ATATGGGGCT ATAATACGTT	240
CGACCTTGGG CAACCGnT	258

(2) INFORMATION FOR SEQ ID NO: 4618:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 216 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:

TCTAATTGAT AGTGAATATA ATTAGAGTTn GAGGCTGGGA CATAAATCCC TAAATTTCA	60
CAGTAAGATA ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACT	120
CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT	180
GCTCCCTCAG GGGTCTCGCC ATTTAATACT ACGTAT	216

(2) INFORMATION FOR SEQ ID NO: 4619:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:

ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGGCAA	60
GCGATTnGTC GTCCTAAAAC AGGTACATAT GCGCTATCTG ACCTAGTCGG TTTAGATATT	120
GCAGTGTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AAACACCCnT ATTTTCATGA	180
TGGTCAAAAT TTGTAAATAC GTTGTTTTGA CAATGGGCGC ACCTCGGACC GTAAAACG	238

(2) INFORMATION FOR SEQ ID NO: 4620:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 249 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:

AACCATTGAA GCACCCCAT T ACGTTTTGGC TGACACGnAC GTATATCGCC TGCCCAAGCA	60
GATGCAGCCT TATTAACACC TGAACCACTT CGAACGCCAC TACCTTTAAG TGACTTCAAC	120
CATTTTTCTT GGATCTTTAG CTGTATGCAT TGCCCTGGAT GCGACCCTTG nCATCAATTG	180
GGAAATGTAA GTGTGCTCCT GCTAACGAAA TTACCTGTAG CACCTGGATT TCCCATCAG	240
TTGACCAGC	249

(2) INFORMATION FOR SEQ ID NO: 4621:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACG	60
TAAATTTAAT CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG	120
TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA	180
AGGTGAATCG AAGAGAAATC ACAAAGTCCG TnTGnTTA CAGGTACGGC AGAACGATAC	240
ACAGTCTCGG GCGATTGTCG AGTCCAC	267

(2) INFORMATION FOR SEQ ID NO: 4622:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:

CAAAAGGTAG TTAAATTAG GAGTGGGAA ATTGATAAGA CCACTAATGA CGATAAAGAT	60
TAAAAGGAnG ACGTTATGAT GACGATTAAA GTTGATCAT TGGGTGTGGT GGTATTCCAA	120
TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC	180
GTAGACATTT CGAAGCAGCG AGTGCGGCAG AAGCATACGG ACTGACAATG C	231

(2) INFORMATION FOR SEQ ID NO: 4623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:

CGAAACCGGC CCGACCCGGA CCnACCCGAG GAAAGGTACC CnAAAGnTGA AGCCCGGGAA	60
AACCACCCAA ACGGCCCACC CAAACCACCC AGAAGTACCC AAAGTGAAGC CCGGAAAACA	120
CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA	180
CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCCAAAGAA GAACCTAAAA	240
AGCCTTCTAA ACCAGTGGA CAAGGTAAAG TAGTAACACC TGTTATTGAA ATCAATGAAA	300
A	301

(2) INFORMATION FOR SEQ ID NO: 4624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:

CGAGGTGCTG CAGAAGGTGT CATTCGTCGT TATTTAATTG AAGAAAAGAA CTACTTAGAA	60
GCTGTGATTG GTTTGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTTA	120
GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT	180
TTTGAAAAAG GGGnAAATCA TAATCATnG GCGATGCCCA AG	222

(2) INFORMATION FOR SEQ ID NO: 4625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:

TGGAAAGTGA' ATCAAAGAGG TAATATCCGT AGTCGAAATG TTGTCTCTCT TGAGTGGATC	60
CTGAGTACGA CGGAGCACGT GAAATTCCGT CGGAATCTGG GAGGACCATC TCCTAAGGCT	120
AAATACTCTC TAGTGACCGA TAGTGAACCC AGTACCGTGA GGGAAAGGTG AAAAGCACCC	180
CCGGAAGGGG AAGTGAAATT AGGAACCCTG AAAACCCGTG TGCTTTACCA AAGTTAnGTT	240
CAAGAGGCCC CGTTTAAATT GGGGTnnAAT TGGCGGTGCC CTTTTTTGGT AGGAATTGAA	300
A	301

(2) INFORMATION FOR SEQ ID NO: 4626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:

GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATACAAT TTACAAATAG	60
CGACAAATTC TCAATTTGTT TTATCCTATG ACCTATTTCA AAACCCAACA GATACTAGAA	120
CATTAATCCC ATTTTTTAnCA ATGATTCAAA ATACCTTCGG TTATTTACCA GAGTATATTG	180
TAGCTGATGC AGGTTATGGT AGTGAGCAAA ACTATATGGC nAT	223

(2) INFORMATION FOR SEQ ID NO: 4627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:

TTGTTGGGGC CCCGCCnGCG nCATTCGCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG	60
GGGCCCCTGA CTAGAATTGA AAAAAGCTTA TTACAAGCGC ATTTTCGTTC AGTCAATTAC	120
TGCCAATATA ACTTCGTAGA TCATAGAACA TTGATTTATT TCCCAGCCTA TTCTTTTCAT	180
AAAAAAAAGA CGGATTAATT ATCCGCTTTT TCCTTATATC T	221

(2) INFORMATION FOR SEQ ID NO: 4628:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:

ATATATTCGT ATTTATAGTA AAATTAAATA AAGAGnATTA TATAACACGA GGTGTAGTAA	60
GTATGAAATT TGAGnAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC	120
GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTAAATCTG TATGTGTGAA	180
TCCACCACAT GTTAAATATG CAGCAGAG	208

(2) INFORMATION FOR SEQ ID NO: 4629:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:

ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG	60
TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTGTGAC GACTAACTA AAGTTCGTGC	120
ACACAATAA GATTGATCAG CTAAAGCTTA CTTCAAATAA AAGAGATATA GCCATTAGTA	180
ACGTTAAAAT AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAGTA	240
TTGATACTnT ATCGAGAGCG TGAGnGAACT GAATACTGCG CTCACGGTAT TACATGCGTG	300
CACTG	305

(2) INFORMATION FOR SEQ ID NO: 4630:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:

TCGACTACCA TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGTGTGACT	60
CCTTGCTATA GTCACCAGAC ATATGAATGT AATTATACAT TCCAACTAG ATAGTAAGTA	120
AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT	180
CAGCTCCACA TGTCACCATG CTTCAnCTn GAA	213

(2) INFORMATION FOR SEQ ID NO: 4631:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:

GAnGTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA	60
TGGCGTGCCT TTTGTAGAAT GAACCGGCGA GTTACGATTT GATGCAAGGT TAAGCAGTAA	120
ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG	180
GAAACCAGGT GATCTACCCT TGGTCAAGTT GAA	213

(2) INFORMATION FOR SEQ ID NO: 4632:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:

GCTTTTAAAT CAAATGATAG CGGAAGGGnA TTTTAAATT ATTCGAACCA TATTTACAG	60
CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTTGGTGC CTTTGCATTA TTCTGGTTTG	120
TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCGAATA	180
TCGAAGCGAA CTTCAAGTTG CTTCA	205

(2) INFORMATION FOR SEQ ID NO: 4633:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:

AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTTCTA	60
CAGACAATGC AAGTTGGGGT GGGCTCTAAC ATAAAGAAnt ACTTTTTCTn TAGAAATTAG	120
TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTGCACA TTAGCAGCGG	180
CTAATGTGTT AAGAACTACT ACAT	204

(2) INFORMATION FOR SEQ ID NO: 4634:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:

GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TGTAGGTAAG	60
AACGTTnGGG CAAGGTATGA GTGGTGGTAT TGC GTTACGT TAGCCCGTCT GATGTAGAAG	120
CTTTTGTGTA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAA CACCAAGAAG	180
AAAAAGCATT CATTAAGCAA ATGCTGGAAG AnCCATGTGT CACACA	226

(2) INFORMATION FOR SEQ ID NO: 4635:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:

CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC	60
GAAGAGTTGT TGAATCATTG TTAAAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTTG	120
AAATAGGTCA TAGGATAnAA CnGTACGGAG AATTTGTCTGC TATTTGTAAA TTGTATCCTG	180
GCTTAAGTTG GCCATTTTTTC ATATGGTC	208

(2) INFORMATION FOR SEQ ID NO: 4636:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:

TTTTTCTTTG TGTTTATTTT TATTTTGAAC GTTTTAGGAC ATAAAAAAAA GTAGACCTTG	60
CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA	120
CGTAAGTTGG CTACCATCGA CGCTAAGAAC CTTTCTTGAC TTGTGACAAT CGCTTGCTTC	180
TTTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG	228

(2) INFORMATION FOR SEQ ID NO: 4637:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:

CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACCTAA GATGGATCCG CGCTGCATTA	60
GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCCT GAGAGGGTGA	120
TCGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGnATC	180
TTCCGCAATT GCGGAAAGCT GTACGGGCAA CG	212

(2) INFORMATION FOR SEQ ID NO: 4638:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 4638:

ATnTnATTAA ATAGAGAACA GCAGTAAGAT ATTTTCTAAT TGAAAATTAT CTTACTGCTG	60
TTTTTTAGGG ATTTATGTCC CAGCCATTTT TGTATTCATA TTAAATTTT GATAATTTTT	120
CAGGAAGCAT TTTAATTTTA CTAATGAAGC CATATTTTTA GATTAACCAA AATTAATATT	180
TACATTTTCCT AACCATTTTT ATGTAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA	240
GTTTAGGATA AAGAGG	256

(2) INFORMATION FOR SEQ ID NO: 4639:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:

AnAGnAACCA CTACATAATA AATCATTAGT GGCTCTTTAT CATTTCTGTC CCACTCCCCT	60
GAGAAGTTTA AAATTTTATA TGTGCGCTTG TTATTTAAG GGAATTAACA TGGTTGTCTT	120
GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAAA TCTAATTCCG TAAAATGCTA	180
AATCTAACCA TCTATTAAAT TTTAAAACC	209

(2) INFORMATION FOR SEQ ID NO: 4640:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:

nGnAAAGGTG AAAAGCACCC CGGAAGGGAG GTGAAATAGA ACCTGAAACC GTGTGTTAC	60
AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT	120
ACGATTTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAAGCATG GTCTGAATAG	180
GTGCGTTTAG TATTTGGTCG TAGCCCGCAG AACCAGGGTG ATCT	224

(2) INFORMATION FOR SEQ ID NO: 4641:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:

CACTCACnCA GATTTTTTAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA	60
AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TTTATTCTAC	120
CGCTGAACTA CTTCTGCATA TGCGGGTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTAnG	180
ATCCTAAGTC TAGTGCGTCT GCCAA	205

(2) INFORMATION FOR SEQ ID NO: 4642:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:

AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGGTTG GGGTGGCTGG ACACGGCACC	60
CTGAGGGAAG GGCACCCGTC ATCAAAAATT CTATTTATAG AATTTTACAG TAATGTGACA	120
GACGGGCAAA GCGAACCATT CAATACGAAG TATTGTATAA ATAGAGAACA GAGTAAGAT	180
ATTTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTTAGG GATTATGTn CCCAG	235

(2) INFORMATION FOR SEQ ID NO: 4643:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:

```
AGnAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA      60
CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA      120
GTTTCGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC      180
ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC      240
CGAAGCCGTG ATACTTTTAG                                     260
```

(2) INFORMATION FOR SEQ ID NO: 4644:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:

```
CAGCAGGCCA CCAAATTGT GTCCGAGAT GTTCATATAA AACTTTATAT AATTCATCAG      60
TTCCTAACAT TTACACCCTC CATTTTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA      120
ATTTATTTTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTCnCTT      180
GTTGGGGGCC CGCGGGCAAG GTnACTAGAA TGAAAAAAGC CTGTTACAG CGATTTTCGG      240
TTCAGTCCAC TACTGGCAAT ATAACTTGTA GAGCTAGGAC ATTGG                                     285
```

(2) INFORMATION FOR SEQ ID NO: 4645:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:

```
GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG      60
CGCTTGnTG GGGGTTCAAC TGGAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn      120
TACGAACGTG TTAAAACAGT ATGGAAGACG AACTTGGAGA CTTACCACAA TGGGTTAGTG      180
ATTTAGATGG TGGCTTTTGA TAAACA                                     206
```

(2) INFORMATION FOR SEQ ID NO: 4646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

```
ACAGTTACCG ATACAACTGA AGATGATAAC GATGCAGATG GTGGCGACGT TGACGTCACA      60
CTTACGGATC ATGATGATTT CACACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA      120
GCGATTCAGA CTCAGATAGT GACTCAGACA GCGACTCAGA CTCAGACAGC GACTCAGACT      180
CnGACAGTGA TTCAGATTCA GACAGCGACT CAGATTCnGA TA                          222
```

(2) INFORMATION FOR SEQ ID NO: 4647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:

```
GTACTATTCG TGTGTGACAA TGTCTTCCA GCATTTGCT AATGAATGCT TTTTCTTCGT      60
TTAATCTTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA      120
GnCGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA      180
CCGAAATTAA TGACAGTCCA                                          200
```

(2) INFORMATION FOR SEQ ID NO: 4648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 4648:

```
CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTTGC      60
ACGCAGGAnG TCAGCGGTTC GATCCCGCTA GTCTCCACCA TTATTTGTAC ATTGAAAAC T      120
AGATAAGTAA GTAAAATATA GATTTTACCA AGCAAAACCG AGTGAATAnA GAGTTTTTAA      180
TAAGCTTGGA ATTCATTAAG A                                      201
```

(2) INFORMATION FOR SEQ ID NO: 4649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:

AGTAAATACA GATGGAATAA ATCTTTTAAG GCTTATAAAC GCTCATCTGn CATTGTAGCA	60
ATTCATGCTT TCAAAAGACG ATATACTACG AACTCCTAC GAACTTGTCC AAGGATTACG	120
AAAAGACCTA AGGTTATGTA ATTGGCCTAA ATTCATAAT CGCTTAAATT CACTTAGTAA	180
AAAGTCTGTG AGTAAGGGTG TATGGAAAGT GGTnAAAT	218

(2) INFORMATION FOR SEQ ID NO: 4650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:

GTGGCGGTGC GACTGTCAGA AGCACGTAA ATTAATGAAA GATACAGTAG GTGCTGATGT	60
AGAAGTAAAA GCCATCAGGT GCGGTACGTA ATTTAGAAGA TTTCAATAAA ATGGTGAAG	120
CAAGTGCAC ACGTATTGGT GCGAGCGCAG GTGTTCAAAT TATGCAAGGT TTAGAAGCAG	180
ATTCnGATTA CTAATATnTA TG	202

(2) INFORMATION FOR SEQ ID NO: 4651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4651:

AGCGGCGGAC GGGTGAGTAA CACGTGGATA ACCTACCTAT AAAACTGGnA TAACTTCnGG	60
AAACCGGAGC TAATACCGGA TAATATTTTA AACCGCATGG TTCAAAAGTA AAAGACGGTC	120
TTGCTGTCAC TTATAGATGG ATCCGCGCTG CATTAGCTAG TTGGTAAGGT AACGGCTTAC	180
CAAGGCAACG ATGCATAGCC GACCTGAGA	209

(2) INFORMATION FOR SEQ ID NO: 4652:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4652:

TGAAGATGCA GGTTACCCGC GACAGACGG AAAGACCCCG TGGAGCTTTA CTGTAGCCTG	60
ATATTGAAAT TCGGCACAGC TTGTACAGGn TAGGTAGGAG CCTTTGAAAC GTGGAGCGCT	120
ACTTGAnTGG TTAGGCGCTG GTGGGATACT ACCCTAGCTG TGTTGGCTTT CTAACCCTGA	180
CCACTTATCG TGGTTGGAGA CA	202

(2) INFORMATION FOR SEQ ID NO: 4653:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:

CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCGGTA	60
TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGCTCT	120
ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG	180
AACCGGTACG TGATCACTCA ACnGn	205

(2) INFORMATION FOR SEQ ID NO: 4654:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:

AGACGAAACG TTGTTGTTGC GAAGATAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC	60
ATTAActGGT GAAGTAACAC CATTATCAGA AGTGCCTGAT CAAGTGTTCA GCGAAAAAAT	120
GATGGTGACG GTATCGCTAT CAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT	180
AAAGTACCAA TGATTTCCCA ACCAAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn	240
CTATTAATCC ACACGGGTTA GAnG	264

(2) INFORMATION FOR SEQ ID NO: 4655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:

GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GGTGATGCG CCACCACAAG	60
CCCCACATTC AAGTGATGCA TGATGTGGAT TATTGTGAGA ATGACTAGCA TGGCCCTGCT	120
AACACAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGTnACGCG	180
AAATCAGTTT GCTCTTGGCT GCAGTAAATC G	211

(2) INFORMATION FOR SEQ ID NO: 4656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:

TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC ATCTTTCTTT	60
GTGTTTGCTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTTGCGG TCTCAATGCG	120
GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGACT	180
ACCATCGACG CTAAGGnGCT TAACTGnTGG GT	212

(2) INFORMATION FOR SEQ ID NO: 4657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:

TGGGTTCGAA nTCCAATTAG GACCCACCAT TAACTTAATA CCTATTGCGG GGCTTAGCTC	60
AGCTGGGnAG AGCGCCTGCT TTGCACGCAG AGGTCAGCGG TTCGATCCCG CTATCTCCAC	120
CATTATTTGT ACATTGAAAA CTAGATAAGT AAGTAAAT TAGATTTTAC CAAGCAAAAC	180
CGAGTGAATA AAGAGTTTTA	200

(2) INFORMATION FOR SEQ ID NO: 4658:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:

TACAGTATAT CGGGAAGACA GGATTCGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT	60
CTACCAAGCT GAGCTACTTC CCGTATAATT AACGCGCCCG ATAGGAGTCG AACCCATAA	120
CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTTATTG	180
AAAAAn	185

(2) INFORMATION FOR SEQ ID NO: 4659:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:

AAGTGTTAGG GGGTTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAGC ACTCCGCCTG	60
GGGAGTACGA CCGCAAGTGT ATAACTCAAA GGAATTGACG GGGACCCnCA CAAGGTTGGA	120
GCAATGTGGTT TAATTCGAAn CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTTGAC	180
AACTCTAGAG ATAGAGCCTT CCCCTTCG	208

(2) INFORMATION FOR SEQ ID NO: 4660:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:

ACGTCGCGAG AACGCAATTA GCTGAAAAAGATTACAACAT TAGAACAAGA TTTAAAGTCA	60
CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA	120
GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTTCTA TTATTTATTT	180
GATAGAAATC ACTTTTTGAT ATGTATTTnT ATGTACAGCT CGTTGAGChC TATTTCCTT	240
ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTTAACTT TATTATTCCG AACTGACATC	300

GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTTGAnT GGTTTTCGTT 360
CTGTC 365

(2) INFORMATION FOR SEQ ID NO: 4661:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:

AAAGTATTTT TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT 60
 CCAATTCTCC TnATGTTGGG GCCCCGCAGT TCAACTACTG CCAATATAGT GTTGTAGTGT 120
 CTAAGACATA AAAGTTCATC TCAGTCACAA TTACTTTATA GCCTATCCAT CATCTTTTCT 180
 ACATGAAATT TTTCCAAGTG ATATATTTT 209

(2) INFORMATION FOR SEQ ID NO: 4662:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:

TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA 60
 AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC 120
 CCAGGTAAAG ATATTGCTGA TGACTATAAA CCTCAGCACT TAAACCAAGG CTGTTATCA 180
 CGCACCTGGT GTTTGCATAC CAGGAACTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG 240
 GCCTAA 246

(2) INFORMATION FOR SEQ ID NO: 4663:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:

AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT 60
 TTAAGGAAGC GATTACAAT CGAGAATCAC AAAGTACAAC TGGTATCGGC GAAGGTATnG 120

CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAAATCTA 180

AAGCAGGCGT AGATTATCAA AGnTTTTGGT ATGCAACCAG CACACT 226

(2) INFORMATION FOR SEQ ID NO: 4664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:

TTCCGTCTCG GCACCATTTT ACGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT 60

CAAGAGGTAT GGGTTCGACT CCTATCGGGC GCGCATTTTT AAATTAATTG AATAACGGGA 120

GTAGCTCAGC TTGGTAGAGC ACTTGGTTTG GGACAAGGGC GCAGGTTCTGA ATCCTGTCTC 180

CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTTT nCAC 234

(2) INFORMATION FOR SEQ ID NO: 4665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:

GTACATCTAA AATCATCCAT GAAGGTTTGT TACCTGAATT ACGGAATGAT TCAACAACCTT 60

CTAAACGTTT AATTnACCAG TAAGTCTTTG CCAAGTAGCT GATTCCAACCT CATCGCGTAC 120

AATTTAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC 180

CATTTTTGCA CGAATT 196

(2) INFORMATION FOR SEQ ID NO: 4666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:

CCGCCGAACA ACTACTTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTTCT 60

TAGATTGTGG TTTTTTAGTT GGTGCCATGC TTAAACCTTT TCATTGATTT CAATAACAGG 120

TGTTACTACT TACCTGTTCC ACGGTTTAGA AGGCTTTTAG GTTCTTCTTG GCAGTGGTAn 180
GGTTTACCAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTG GATTTC 226

(2) INFORMATION FOR SEQ ID NO: 4667:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:

GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGAnAA CCGGTGATCT ACCCTTGGTC 60
AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGAÆ CGACTTACGT TGAAAAGTGA 120
GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTC 180
CGAAATA 187

(2) INFORMATION FOR SEQ ID NO: 4668:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:

CTAAGTGGAG TTGTCACAAC ATCTTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTTT 60
GAAAATGCTT TTGCCAACGT TTTATAAATA TCCCAGTCTG AACGCGATTC CCATAACGGA 120
TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGn 180
TT 182

(2) INFORMATION FOR SEQ ID NO: 4669:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:

AGTTACGTTA AAAGATGAAA ACGACAAAGT TTTAAAAACA GTTACAACAG ATGAnAATGG 60
TAAATATCAA TTTACTGATT TAAACAATGG AACTTATAAA GTTGAATTCTG AGACACCATC 120
AGGTTATACA CCAACTTCAG TAACTTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT 180

TT

182

(2) INFORMATION FOR SEQ ID NO: 4670:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:

```
GGGGCAAAGT CATTnCATAG ATTAATGGTT CTCCGATACC TAGGAAACCA ACTGGCAATG      60
CACCTTTTAA AGTATTACGT AATGTTGTGT TCGTTTACA TCTTACCCAA AGTGCTAATG      120
CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAGACCTG      180
ATTGG                                           185
```

(2) INFORMATION FOR SEQ ID NO: 4671:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:

```
CTGACGAACG AGAAAAGAGC GCAACGATTT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA      60
GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTCGATGGTA      120
GCCAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG      180
CATTGAGACC GCAAGGnTnT                                           200
```

(2) INFORMATION FOR SEQ ID NO: 4672:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:

```
CCCGGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCATCGC      60
ATCCTGGGCT GTAGTCGGTC CCAAGGTTG GGCTGTTTCG CATTAAAGCG nACGnTGCTG      120
GGTTCAGACG CGTGAGCAGT CGGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC      180
```

TGTCCTTAGT ACGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTCG TGCCACGCAT 240
 AGTGGGTAGT ATGTGTGGAC G 261

(2) INFORMATION FOR SEQ ID NO: 4673:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 184 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:

ATAGGGCGTT TAGTATTTGG TCGTAnCCAG AAACCAGGTG ATCTACCCTT GGTCAGGTTG 60
 AAGTTCAGGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA 120
 ACTGAGGGTA GCGGAGAAAT TCCAATCAAA CCTGGAGATA GCTGGTTCTC TCCGAAATAG 180
 CGTT 184

(2) INFORMATION FOR SEQ ID NO: 4674:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:

CCCAGTCAAA CTGCCCCGCT GACACTGTCT CCCACCACGA TAAGGTCGTG GGTGAGAAA 60
 GCCAACACAG CTAGGGTAGT ATCCCACCAG CGTnCTCCAC GTAAGCTAGC GCTCACGTTT 120
 CAAAGGCTCC TACCTATCCT GTACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA 180
 AAGCTCCACG GGGTTCTTTC CGT 203

(2) INFORMATION FOR SEQ ID NO: 4675:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:

nnGTTTGTAATAA ATAATATGGT GGAGACTAGC GGGATCGAAC CGCTGACCTC CTGCGTGCAA 60
 AGCAGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT TAgTATAT CGGGAAGACA 120
 GGATTCGAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC 180

TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTA

229

(2) INFORMATION FOR SEQ ID NO: 4676:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:

TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCATTA TTACCTCAAT ATGCTTGTC	60
TCAGTTGCCT TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC	120
TTACAAATTT AGTGTGCnGA GCGTCTTATT TTTATACTTT AAAAGTCGTA TTGGTTGT	178

(2) INFORMATION FOR SEQ ID NO: 4677:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:

GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG	60
TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG TAACACTGAA	120
TGGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA	180
AAATCCCAAT CGAACCCTGG GAGATAAGCT TGGGnTCTCC TCCCGAAAAT AAGCCTTTTA	240
GGGGCTTAAG CCTCCAAAGT GGATGATTTA ATTTGGAAg TAAAAh	286

(2) INFORMATION FOR SEQ ID NO: 4678:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:

CACACGGCTT ATGGTAACAA AAAATTCCTT TGGAGCATTA TGGAGCGGAA GATAGGTTTA	60
CACCTATACC TCGTTCCGGA AGGAnTGTTT TAAAAGTGAA CTACTCCCGC AATATTAAAT	120
ATGGAGCGGA GATAGGATTT ACACCTATAC CTCATTCCAG AGGATGTATT CTAAGA CTE	180

AATACTCCCC ATATATTAAA TATGGAGCGG AGATAGGATT GACCATACn

229

(2) INFORMATION FOR SEQ ID NO: 4679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:

ATGACTGCTT TTTATTATAC TTTACATTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT	60
CGCCAAGCCA TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG	120
ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG TTC	173

(2) INFORMATION FOR SEQ ID NO: 4680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAAATCCA	60
TTAACTGGAG AAATTATTAG TAAAGGTGAA TCGAAAGAAG AAATCACAAA AGATCCCATT	120
AATGnATTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTTGAT	180
CCC	183

(2) INFORMATION FOR SEQ ID NO: 4681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:

CGGTGCTTTC ACTTTCCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGCnTTAGG	60
AGATGGTCCT CCCAGATTCC GACGAATTTC ACGTGTTCG TCGTACTCAGGATCCACTCA	120
AGAGAGACAA CATTTTCGAC TACAGGATTA nTACCTTCTT TGATTCATCT TTCCAGATGA	180
TTCGTCTAAT GTCGTCCTTT GTA	203

(2) INFORMATION FOR SEQ ID NO: 4682:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:

```
GGGTCACACC TGTTCCCATG CCGAACACAG AAGTTAAGCT CCTAGCGTG CGATGGTAGT      60
CGAACTTACG TTCCGCTAGA GTAGAACGTT GCCAGGCAAA AAGTGGGATG CGATGGAGCC      120
GCATTGGAGA CCGCAAGCCT CTGTTCTTTG ATGTCTAAAA CGTnCAAAAT AAAAGCGAAC      180
ACAAAGA                                           187
```

(2) INFORMATION FOR SEQ ID NO: 4683:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:

```
GGCTACACTG GTCATGATGC TGCTAAACTA CGTGATTATn ATGAAACACA TCATGCTTTG      60
TCTGGATATG AAATGATTGA CGCAGCAAAG GTGCCATTGC AACAAATGAA GTCAATGCTG      120
CGATGGGTAT ATTTGTGCAA CGCCAACAAC TGGTTCCTCC GGTACCATCC CGGTGCAGTT      180
TTAAATT                                           187
```

(2) INFORMATION FOR SEQ ID NO: 4684:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:

```
AGTGCCAAGG CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA      60
AACCGTTATT AATCTTGTGA GTGTTCTTTC GAACACTAGC GATTATnTCT TATGAATTCA      120
AGCTTATTTA AAACCTTTTA TTCACTCGGT TTTGTAAAAT CTATATTT      68
```

(2) INFORMATION FOR SEQ ID NO: 4685:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:

```
ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTTGGGA CCAAGGGGTC GCAGGTTCGA      60
ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTTATGG GGGCTTAGCT CAGCTGGGAG      120
AGCGCCTGCT TTnCACGCAG GAGGTCAGCG GTTCGATCCC GCTAGTCT      168
```

(2) INFORMATION FOR SEQ ID NO: 4686:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:

```
ATGATTCAAG CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT      60
TTACTTACTT ATCTAGTTTT CAATGTACAA TTTCTTTTGA GTCAAGCGCT CGCATACTGC      120
nTTATTTTCA AAAAATCAAA TGCTCATTTA CAAAAGTAAA CTCCGCTTTT AATT      174
```

(2) INFORMATION FOR SEQ ID NO: 4687:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:

```
TGTTGTTGAA TATGAAGAAG ATACAAACCC AAGTGGTGGT CAGGTTACTA CTGAGTCTAA      60
CTTAGTTGAA TTTGACGAAG AGTCTACAAA AnGTATTGTA ACTGGCGCAG TGAGCGATCA      120
TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA      166
```

(2) INFORMATION FOR SEQ ID NO: 4688:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:

AGAACCTTAC CAAATCTTGA CATCCTTTGA CAACTCTAGA GATAGAGCCT CCCCTTCGG	60
GACAAATGAC AGTGGTGCAT GGTGTGCGTC ACTCGTGTCT GAnATGTTGG GTTAAGTCCC	120
GCAACGAGCG CAACCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG	180
GTGACAAAC	189

(2) INFORMATION FOR SEQ ID NO: 4689:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 227 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:

TAACCACTCC TCTTAACCTT CCAGCACCGG GCAGGCGTCA CCCCTATACA TCACCTTACG	60
GTTTAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTCAC TGCGGCTCTT	120
CTGGGCGTTA ACCCTAAGAn ACCCTTCTCC CGAAGTACGG GGGCATTTTG CGAGTCCTAA	180
CGAGGTCGTC GTCACCTAGA TTCTCATCTT GATACTGTGT GGTTCGG	227

(2) INFORMATION FOR SEQ ID NO: 4690:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:

AGATAATGCA CCATCAACTA ATGGATATTT ATGTCCAGTT GGGGGCCAGA AATCATAAAC	60
GTCTTCAGTG TAAGCAACAG CATCTTCATT TnGCAGCCAA AATGCTTGGA TTATGTGCAA	120
TAACCATCGC AACTGCGCCA CACCTTGTGT TGGCTCGCCG CCTGAAGGG GGTG	174

(2) INFORMATION FOR SEQ ID NO: 4691:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:

TTTTTTTTTTA AAAAAAGGGA AGGGAAAAAnA AAAAGGGAAA AAAATTTAAC CCAAGGGTTT	60
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TTAAAGGGGG CCCAATTTTT CCCAAAAAA AAACCCTTTG GGTAAATTT TTTTAAAAA	120
CCCAACCCAA AAnTTTTTTA AAAAGGGTTT TGGGCCCCC TTGGGAAAAA TTTTCCCGG	180
GTTAAATTTT TTTAAAAAGG GTTCCTTTT AAATTTTGGG AAAAACCCCC TTTTTTTTTT	240
TTAAGGGAAT TTA AAAAATT TAAGGCCCTC CCCTAAATTA AAATTAAAGG TGGGAAAAA	300
AAAATTAATT AAAnAACCCA TTTTTTTTTT TTAATTTTTT AACCCAAAGG GGGTAATTTG	360
GCC	363

(2) INFORMATION FOR SEQ ID NO: 4692:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 210 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:

TAGTGCAAT TTTATTGATA TTTGCAATTA AACTGAAATT TAATTTTTCG GATGTATTTT	60
nTTTACTTAA AGTAAATAG AACACGATTT TGATGTCTGG GAATAGTGGA AATGATAAAA	120
ACTACTAATG ATTGATTAAG TAGTGTTCT TAACATTAGC CTCTCTAAT TGTTACTTAA	180
AAATAGGAAT ACATGAGTAA AACTCAnTGG	210

(2) INFORMATION FOR SEQ ID NO: 4693:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:

ATAGTAGTAA AGTATTTTCT TCCAAACATT TATTTTGATT AAGTCTTCAT CATTAGTATT	60
CTCAGCTCCA CATGCACCAT CTCCACCTC AACCTATTAA CCTCATCATC TTTAGGATCT	120
TATAACCAAT TGGAAATCTC ATCTTGAGGn nGCTTCATCT TAGATGCTTT CACACTTATC	180
CCTCCACACA TAGCTACCCA GCTATCCGT	209

(2) INFORMATION FOR SEQ ID NO: 4694:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4694:

GCACATTAAC CnAAGCACCA GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG	60
CATGTGACGG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAAAA	120
GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT	180
ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG	222

(2) INFORMATION FOR SEQ ID NO: 4695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTAT CTAAATGACT ACCAATTAAA	60
TCTATTTCTT CTATTGTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT	120
TCTTCAACTA AGTCACGATA TAATGTTTTT GAATTTTCG	159

(2) INFORMATION FOR SEQ ID NO: 4696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:

AATATGGTAG TTTTAACTT ATCTATTAAG GTACAATTGA CCAAATCGAT AAAAATA	60
ATACGTATCG TCAGACAATT TATGTCAATC CAAGTGGAGA TAACGTTATT GCGCCGGTTT	120
TAACAGGTAA TTTAAACCA AATACGGATA GTAnTGCATT A	161

(2) INFORMATION FOR SEQ ID NO: 4697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:

CCAAACTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT	60
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GATGGGTGTT AATGAACATG GCGTTGCCAT TTCAACACAA TATTTCCGAG GTTATAGTTC	120
ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA	170

(2) INFORMATION FOR SEQ ID NO: 4698:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:

CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTA	60
TTGGGCGTAA ACGCGCGTAG GnGTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA	120
GGGTCATTGG AAACCTGGAAA CTTGAGTCAG AAGAGGAAGT G	161

(2) INFORMATION FOR SEQ ID NO: 4699:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:

TAAATCTTCA TCAATATGAT CTAACCAATA TTGATAAAAC CTTGATGTGT TTCGTGTCAA	60
TGACATACCA TATCGACTAG GTACCTTTTT AGAATGTTGA TTAATACAA CAAATATCAT	120
GGGCAAGGTC ATCTTGCAAA ATGGATTCGA TTCAAGTGGG AGGGnCGATG ATGGACGTGC	180
TGCATGCACT GATGACCCTT TTTGCCCAT CTGGCAAATC CCACCATGAA ATGACTGACG	240
CGGACGCn	248

(2) INFORMATION FOR SEQ ID NO: 4700:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 175 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

CCCGACGAAG CGAACGTTTG GCACTGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT	60
GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT	120
GATATTGAAA TTCGGCACAG nTTGTACAGG ATAGGTAGGA GCCTTTGAAA CGTGG	175

(2) INFORMATION FOR SEQ ID NO: 4701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:

TACAGGGTAG TGAGATTTTCG AAACAATATG GAGAAGCAGG ACTTCCTGGA AAATACAATT	60
AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTCTTGCA GGCATATGCA CCGAAAGCTT	120
AATGATTCAT CATACTGGAG ATGCGAATGA CTATGTTGGG TAAAGGATTT ATCTGGT	177

(2) INFORMATION FOR SEQ ID NO: 4702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATAG GCAAATCCGG TACTCGTTAA	60
GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA	120
GAAAAGnCTC TAGATAGAAA ATAGGTGCCC GTACCG	156

(2) INFORMATION FOR SEQ ID NO: 4703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:

CTTGAAAAAG ATGTTTATTC TGTGTAAGTA ATTGACTTAC GTACTGTTCA ACCAATCAT	60
GTTGACACAA TTGTAGCTTC AGTTGAAAAA ACTGGTCGTG CAGTnGTCAG CAAGACGCAC	120
AACGTCAAGC TGGTGTTGGT GCAGCAGTTG TAGCTGAATT AAGTGA	166

(2) INFORMATION FOR SEQ ID NO: 4704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:

GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG	60
ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT	120
GGCAACGTTC TACTCTAGCG GAACGTAAGT TCG	153

(2) INFORMATION FOR SEQ ID NO: 4705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:

AGGTAGAGCA CTGTTTGGAC GAGGGGCCCC TCTCGGGTTA CCGAATTCAA ACAAACTCCG	60
AATGCCAATT AATTTAACTT GGGAAGTAG ACACATGGGT GATAAGGTCC GTATTGAAA	120
nGGAAACAGC CCAGACCACC AGCTAAGGTC CCAAATATA TGT	163

(2) INFORMATION FOR SEQ ID NO: 4706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:

TAAGGTTGGG ATTGTTTGTG GGCTCGTTGC CACCCATTGT ACGGCACTCA TCAnTTCAAG	60
CCACCAGCTA CAGTATATCT CCTTGACCAG CCATAATTTG ATTGGCTGA GTCGCGATGG	120
TTTGTAATCC TGATGAGCAG TAGCGATTCA TGTTTGACn GTACCCGTCA GATATCCGCA	180
GCAATGCAAT GTTGTGCAAG TTT	203

(2) INFORMATION FOR SEQ ID NO: 4707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:

CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTTCCAGA GGAGGCTCGT CCGCTCTGGG	60
TTAGTCGGGT CCTAAGCTGA GGCGCAGnGT AGGCGATGGA ATAACAGGTT GATATTCCTG	120
TACCACCTAT AATCGTTTTA ATCGATGGGG GGC	153

(2) INFORMATION FOR SEQ ID NO: 4708:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:

nCTATAATGA ATAAATAATT TAGAAATATG CTTCCGATTG TTCGATGCTT TAATTCAGTT	60
AGAAGCATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTTT GTATTGACTG	120
TATGTCTTTG GATAGAGTTA CAAACTTATT	150

(2) INFORMATION FOR SEQ ID NO: 4709:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:

AAAATTCGGG TTCTCAAATC ATCGGAACAT AACAAAACAA CCTAAGCAAC ATGTAGGCCG	60
TTGTCACCTA ACTTCTTGTT TTTCCGATGA CAGCTTCTA TnAGAGAATG TCATGATTAT	120
TTTATATTCA CTTCAATGTT ATCAGTATTA GTGCCA	156

(2) INFORMATION FOR SEQ ID NO: 4710:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

GTTGATATTC CTGTACCACC TATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC	60
GAAAnGTGCGA TTGGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTA	120
TCGTAAAGGC TGAGCTGTGA TGGGGAGAA	149

(2) INFORMATION FOR SEQ ID NO: 4711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:

TTGACTTCAA TACCATGGGC CAGGTACnCT TTAAATGTTG TTGTCTCAGT TAATATTAAT	60
TGGCTTTTCT TTTGCATAAT TGACAATGGC TTCTGCCAAT GGGTG TTCAG AATCTTTTTC	120
AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG	160

(2) INFORMATION FOR SEQ ID NO: 4712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:

ATAGTGAACC AGTACCGTGA GGACnAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA	60
CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC GTGCCTTTTG	120
TAGAATGAAC CGGCGAGTTA CGATTTGATG C	151

(2) INFORMATION FOR SEQ ID NO: 4713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:

ACCAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC	60
CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGnGGGTA GCGGAGAAAT TCCAATCGAA	120
CCTGGGAGAT AGCTGGTTCT CTCCG	145

(2) INFORMATION FOR SEQ ID NO: 4714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:

TGTnACGCAG AGATCGCGGG TTCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA	60
TAGCGATGTA CCTATAATAA TGGAGGAATA CCAAGTCCG GCTGAAGGGA TCGGTCTTGA	120
AAACCGACAG GCCTTAACGG GCCGCGGGGG T	151

(2) INFORMATION FOR SEQ ID NO: 4715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:

TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT	60
GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACG TGTAATTTTA CTTTGnAATA	120
CTTTAAAAAA ATAAGACACT TTGCCAACTT G	151

(2) INFORMATION FOR SEQ ID NO: 4716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:

GCTGTCATCG GAAAAACAAG AAGTTAAGTG ACAAGGGTTT ACATGTTGCT TAGCTTCTTT	60
TATTATGCGT AATGATGTAA AAAGACGAAT ATTCATTTGT TTGTAAAAGT GGCATTTCTA	120
TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC	152

(2) INFORMATION FOR SEQ ID NO: 4717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:

GGATACTAGT AAAACCATAT TTAGTAAATA CAGATGAnT AAATCTTTTA AGGCTTATAA	60
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ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAGAC GATATACTAC GACACTCCTA 120
CGAACTTGTC CAAGGATTAC GAAA 144

(2) INFORMATION FOR SEQ ID NO: 4718:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:

ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTTGT CACCGAGTC 60
AACTTAGAGT GCCCAACTnA ATGATGGCAA CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA 120
CTTAACCCAA CATCTCACGA CACGA 145

(2) INFORMATION FOR SEQ ID NO: 4719:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:

AAATACCTTT CCACGATCTT CAGCTGGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT 60
CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAACCTGTA ATGGTGTCTG 120
ACACnATGCC ATTTAAAAAT AGCATACCGG CAAAGC 156

(2) INFORMATION FOR SEQ ID NO: 4720:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:

TTAAATCGAG TCTCTTTTAC AGGTCCATAT TTTGTTACGT ATCGACCGGT GGCTAACTAC 60
GTCTCCTGTT TCTGGATTCT TAATTGCGGT TTAAGGGAAC TTCTTCTTTC TCTCnGTTGG 120
TAACTCGGAT CAAATTCGTC TCGATGACCT GG 152

(2) INFORMATION FOR SEQ ID NO: 4721:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:

CACTAGTTCA AGTTCAAGTG GCGACGATTG GTATTTTACA AGAATTTTAT CAACAAGGAT	60
TTAATTAGCT TAAACGCnGC AATCCCTGTG TTACTAGGGC GGATAEATT GGTACCACGG	120
TTACAGCTAT CTTAGCTAGT TTAGCC	146

(2) INFORMATION FOR SEQ ID NO: 4722:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:

CCACACCAAT ATTTTGCGCT AAGTAnATCG CATTAAACGT TTGTCTTCCG CCATTTGAGC	60
CACACTGCTC CAGCTCATAG CGCTATATCG CAGGGAATAA TCATTCCGCC ACCACAACCC	120
TAACATTACC CAGCCATACA GCCATACCAG GGCCAC	156

(2) INFORMATION FOR SEQ ID NO: 4723:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:

ACGGTCTTGC TGTCACCTTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn	60
GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG	120
AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A	161

(2) INFORMATION FOR SEQ ID NO: 4724:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:

CAGAAAGCTC ACGGGGCTTT CGTCTGTCGC GGGTAACCTG CATCTTCACA GGTACTATGA 60
TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTTCGT GCGGGTCGGA 120
ACTTACCCGA CAAGTAATTT CGCTACCTTA GGACCGTAT AGTTA 165

(2) INFORMATION FOR SEQ ID NO: 4725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:

GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCC CTCAAGATGA nATTTCCCAA 60
CTTCGGTTAT AAGATCCCTC AAAGATGATT AGGTTAATAG GTTCGAGGTG GAAGCATGGT 120
GACATGTGGA GCTGGACGAA TACTAATCG 149

(2) INFORMATION FOR SEQ ID NO: 4726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 4726:

TTGAATTTTT GAAAAAAAAA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA 60
ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATTT 120
GCAGATAAAA TTGTCATCAG TGGTTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT 180
CAGCATGCCG GTGTTCTGG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA 240
GAnCGGTAAA GTAGACAnCG GTAGTATACT GAAAT 275

(2) INFORMATION FOR SEQ ID NO: 4727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:

ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAAA TAAGTTTTGT 60

AACTCTATCC AAAGACATAC AGTCAATCA AACATTACG TATCTTTACA ACAGTAATCA 120
TGCATTCTAT GATGCTTCTA ACTGAATnA 149

(2) INFORMATION FOR SEQ ID NO: 4728:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:

GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA 60
TGACAATTAA TAAAGAACCG TTCTTGGCGC AGCACAATGG GCGCTCATG GCAGACTTTT 120
GTGATGCTGA CTTAAAGTAA ACTATTAGAT ATTGnGTG 158

(2) INFORMATION FOR SEQ ID NO: 4729:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:

TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTCTG ATCTGGACCA TATTTTTTTTA 60
TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTT GAnCGCACGT 120
GCCCTCCCAT ACCTCGGG 138

(2) INFORMATION FOR SEQ ID NO: 4730:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4730:

TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTCTGG ATTTGTCTGA ATTCGTAACC 60
GAGAGGCCCC TCGTCCAAAC AGTGCTCTAn CTCCAATAAT CATCACTTGA GGCTAGCCCT 120
AAAGTATTTT GGAGAGAACC AGCTATTTCC AGTTCGATTG GAATTTCTCC GCTACCCTCA 180
GTTTCATC 187

(2) INFORMATION FOR SEQ ID NO: 4731:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:

```
CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA      60
AGCTGGGTTC AGAACGTCGT GAGACAGTTC GGTTCCTT CCGTCGTGGG CGTAGGAAAT      120
TTnAGAGGAG CTGTCCT                                           137
```

(2) INFORMATION FOR SEQ ID NO: 4732:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:

```
TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA      60
TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTT      120
TCTTCAACTA AGTCACG                                           137
```

(2) INFORMATION FOR SEQ ID NO: 4733:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:

```
TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA      60
TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT      120
TCTTCAACTA AGTCACG                                           137
```

(2) INFORMATION FOR SEQ ID NO: 4734:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:

AAAACATAAA TACAAAATA TAGCTATTAC TATAAAAAC AGCAGTAAGC ATATTTCCAA	60
ATTGCAAATT ATCCTACTGC TGTTCTTTTT GGGCAGTGGG nACAGCAAAT GATATTTTCG	120
ACAAAATTTA TTTCGTCGTC CCACCCCAAC TTG	153

(2) INFORMATION FOR SEQ ID NO: 4735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:

TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCCATC CCCAACTTGC ACATnATTGC	60
AAGCTGACTT TTCGTCACTT GCTTTGTTGG GGCCCCGCCA ATAAGCGTTG TAGTGCCTAG	120
TACTTTGATT GATGTCCAAG TT	142

(2) INFORMATION FOR SEQ ID NO: 4736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:

ATGTTATTCA AAGTAAATTG CTTTGCCTGA TTTTGCAGAC TGATAAATCG CTTCAAGAAT	60
TTTTGTAACT ACCATTGCTT GTTCCGGTTT CACAACTGGT TCAGTATCAT TTACAACnGC	120
ATCAATCCAA GCTTTTG	137

(2) INFORMATION FOR SEQ ID NO: 4737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:

GGTCGTTTAG TATTTGGTCG TACACCGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA	60
---	----

AGTTCAGGTA ACACTGAAAT GGAGGACCGA ACCGACTTAC GTTGAAAAnT GAGCGGATGA 120
 ACTGAGGGTA GCGGAGAAAT TCCA 144

(2) INFORMATION FOR SEQ ID NO: 4738:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:

GGGTAGCTAT GTGTGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA 60
 TGAGATTTCC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTGAGGTTG 120
 GAACATGGTG ACATGTnATC TGCTTTTCTA ATCATAC 157

(2) INFORMATION FOR SEQ ID NO: 4739:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:

GCTTTATGTC TAAACGTCA AAATAAAAAG CAAAACAAA GAAAATGGC TTGGCGAAGT 60
 GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAnATG 120
 AGTAAGTGAG AGCCGAAGAG AGGGA 145

(2) INFORMATION FOR SEQ ID NO: 4740:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:

TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTGGTCT 60
 CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGTCTTTTC TCGTTTCGTC AGATCAAACG 120
 TTCACTTCG CCAAGCCATT TTTCTTGTGT TTATTTTATT TGACGTTTAG ACATAAAAAA 180
 GAGACCCACG TTCAACTTGC CnGCACGTT TACTCTGCGG AnTAGTGGCT ACCA 234

(2) INFORMATION FOR SEQ ID NO: 4741:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:

GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAC GGCGCATTAC CAGAGTTGCA	60
TGGTCAAAAT ATATTGTTGT CATTTGAAGA TGGACGTGTA CAAAATGCG TGTTACGTGA	120
TCATGATACT GTCAn	135

(2) INFORMATION FOR SEQ ID NO: 4742:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:

ACCCTGGTAC AGTTGAATTC AGGTAACT GAATGGAGGA CCGAACCGAC TTACGTTGAA	60
AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGA GAnAGCTGGT	120
TCTCTCCGAA ATAGCTTTAG GGCTA	145

(2) INFORMATION FOR SEQ ID NO: 4743:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:

TGTCATTCAA GTAGCGAAAG AATTTGCGCA AAACGCTATC GATACBAAG GGGCGTTCAA	60
TGATTATCAT GGGTGC GGGT ATTAACCATT GGTTTAACTC AGATACGATT TATnGTGCAA	120
TCTTAACTT AGTTATGGTA TGTGGCGTCA A	151

(2) INFORMATION FOR SEQ ID NO: 4744:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:

TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC	60
AGGCGATAAA ATCAnAGATG GTGCATCTTG GTTAGGCGAT AAAATCGGCG ATGTGTGGGA	120
TTATGTACAA CA	132

(2) INFORMATION FOR SEQ ID NO: 4745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:

CGTGCGCTCT AACCAGCTGA GCTATAGGCC CATTAATTTG AATGAACAAA CATTCAAAAC	60
TGAATACAAT ATGTCAGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT	120
AGAAAGGAGG TG	132

(2) INFORMATION FOR SEQ ID NO: 4746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:

GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTCAGA CAGCGATTCA	60
GATTCAGACA GCGATTCAGA TTCAGATAGC GATTCAATT CCGACAGTGA CTCAGATTCC	120
GACAnTGACT CGGATTCA	138

(2) INFORMATION FOR SEQ ID NO: 4747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:

CATTATTGTA AACTGAACTT TTCGTCACTT GCTGGTGnTT GGGGACCCCA CCAACTTGGC	60
ACATTATTGG TAAGCTGACT TTTCGTCACT TACTGTGTTG GGGCCCCGCC AACTTnATT	120

GTCTGTAGAA ATTGGGAATC CAATTTCTCT ATGTTGGGGC CCACACCCCA ACTCGACATT 180

GCCTG 185

(2) INFORMATION FOR SEQ ID NO: 4748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:

ACCGAATCCC TTCAGACCGG TACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGACAGT 60

ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA 120

AGGATCCTAA ATATAATTTT ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG 173

(2) INFORMATION FOR SEQ ID NO: 4749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:

ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTTAAC TGGGCAAGCG ATTGGTCGTC 60

CTAAAACAGG TACATATGCC GGCTATCTEA CCTAGTCGGT TTAGATATTG CAGTGTCTGT 120

AATTAAAGGG CATGCAACCA AGTAnCTGAG GAAACAACCTT ATTTTCATGG TGTCAAAAAT 180

TGnTAAATAC GGTGTTTGAC AATTGCGCAC CT 212

(2) INFORMATION FOR SEQ ID NO: 4750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:

AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAAGAGT TTAAATAG CTTGAATTCA 60

TAAGAAATAA TCGCTAGTGT TCGAAAGACn GCAGCAAGAT TAATAACGCG TTAAATCTT 120

TTTATAAAAAG AAAACGTTTA 140

(2) INFORMATION FOR SEQ ID NO: 4751:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:

ATTGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTTT	60
GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTCAT GCTAGATGCT	120
TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA	180
TCCG	184

(2) INFORMATION FOR SEQ ID NO: 4752:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:

GGGATCTTCC GCAATGGGG AAACTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT	60
CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG CACATCTnA	120
CGGTACCTAA TCA	133

(2) INFORMATION FOR SEQ ID NO: 4753:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:

GTATGCTGTG TGGCTTGTCa TGTTGGGGTT TGGTGGCGa CCTGATTATT CCTGCGnTAT	60
ACGCTATGGC TGGAGCAGTG TGGCCAAATG GCGGAAGACA AACGTTTAAT GCGATCTACT	120
TGGCGCAAAA TATTGGTGTG GCTGTCGGTG CTGCAATGGG CG	162

(2) INFORMATION FOR SEQ ID NO: 4754:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:

AATTCGATTC CCTTAGTAGC GGCGACGAAA ACGGGAAnGA GCCCAAACCA ACAAGCTTC	60
TTTGGGGGTT TGTAGGACAC TCTATACGGG GTTAACAAAG GACGACATTA GACGAATCAT	120
CTTGGGAAAG ATGA	134

(2) INFORMATION FOR SEQ ID NO: 4755:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:

AGAGTGCgTA ATAGCTCACT AGTCGAGTGA CACTGCGCCG AAAATGTACC GGGGCTAAAC	60
ATATTACCGC AAGCTGTGGA TTGTCCTTTG GACATGGCTA GGAGAGCGTT CTAAGGGCGT	120
TGAAGCATGn ATCGTAAGG	139

(2) INFORMATION FOR SEQ ID NO: 4756:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:

GGTCATTGGA AACTGGAAAA CTTGATTGCA GAAGAnGAAA TTGGAATTCC ATGTGGTACC	60
CGTGAAATGC GCAGAGATAT GGAGGAACAC CAGTGGCCGA AAGCCACTTT CTGGTCTGTA	120
ACTGGACGCT GGATGTGCCA AACCTGGGGG ATCAAACAGG TTA	163

(2) INFORMATION FOR SEQ ID NO: 4757:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:

CATGAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG	60
TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGACATCACAnGAT	120
TAATACCGCG TTTAATCTTT TATAAAGGAC CGTAACTTCA	160

(2) INFORMATION FOR SEQ ID NO: 4758:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 177 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:

TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG	60
GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT	120
ACTGCTGTTC TCTATTTATA CCAnATTACT TTCGTAATTG TTAAAATTTT AAAAGGA	177

(2) INFORMATION FOR SEQ ID NO: 4759:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:

CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG	60
ATTCCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACA ACnTTATGGG	120
ATTTGCT	127

(2) INFORMATION FOR SEQ ID NO: 4760:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:

GGGCCCCTCG TCGGGTTACC GAATTCAGAC AACTCCGnA ATGCCAATTA ATTTAACTTG	60
GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA	120
AGTCCCAAAT ATATGTTAAT GAAAG	145

(2) INFORMATION FOR SEQ ID NO: 4761:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:

TAAACAAGGC GCGTTGGGCC TATTCCTGCG GGCTCTTCTG GCGGTTAACC CTAAAGAGCA	60
CCCCTTCTCC CGAAGTTACG GGGTCATTTT GCCGAGTTCC TTAACGAGAT TGCTCGCTCA	120
CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTTCTTCA AGCTTCCGCA	180
TTAACACACC AAAACAGCTC CCACCACCAC TAnATCGAnC AACACTAG	228

(2) INFORMATION FOR SEQ ID NO: 4762:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:

TnGCCAAATC TTAGTAGTCG CTTGGTTCGG TTGTGGTGCG ACAGCTGTGA AATCATCACT	60
ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGCGTT GCAACAGCTT GAATTGTATC	120
AGCAGGGTTG	130

(2) INFORMATION FOR SEQ ID NO: 4763:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:

CAACTCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTTCCG TCATGGGTAG	60
GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA	120
GTTACATCG ACGGGGAGGT TTGGCACCTC G	151

(2) INFORMATION FOR SEQ ID NO: 4764:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4764:

```
ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCCGC      60
CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTTACAAG CGCATTTTCG TTCAGTCAAC      120
TACTGCCA                                     128
```

(2) INFORMATION FOR SEQ ID NO: 4765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:

```
AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC      60
TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG CGGATGGCCC      120
TTTCCATGTG GnAAC                                     135
```

(2) INFORMATION FOR SEQ ID NO: 4766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

```
GATTCTCACC CGTCTTTCGC TACTCACACC GGCATTCTCA CTTCTAAGCG CTCCACATGT      60
CCTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCCTA CCATTGTCCA AAGGACAATC      120
CACAGC                                     126
```

(2) INFORMATION FOR SEQ ID NO: 4767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:

```
TTAATAGTTT TATAAGAGAG GTGTTTGATC TTGAGCTAAC CACnTCATTC GAGTACTGTC      60
```

ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT 120
GATTTTAAAC 130

(2) INFORMATION FOR SEQ ID NO: 4768:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:

GTTAACCCTA AAGAGCACCC CTTATACCGA AGTTACGGG TCATTTTGCC GAGTTCCTTA 60
AnGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG 120
TAGGGCACCT ATTTTCCTAT CT 142

(2) INFORMATION FOR SEQ ID NO: 4769:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:

CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACCTCC 60
CGTCGATGTG AACTCTTGnG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC 120
GTTGAGCGAT GGCCCT 136

(2) INFORMATION FOR SEQ ID NO: 4770:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:

CTAAAAGTTG TATTTTAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA 60
ACCGTTAAAC AATGCATAGT TTGCTTAACT TCCAATATTG ACTCATCATT ACAATTGACA 120
TAGAGCTATT AAGCGTnGCC ATGAG 145

(2) INFORMATION FOR SEQ ID NO: 4771:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:

TCGAGTGACA CTGTGCGCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT	60
GTGCCTTTGG AAATGGTGAG GnGAGCGTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC	120
ATGTGGGA	128

(2) INFORMATION FOR SEQ ID NO: 4772:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:

GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTTGGCTA	60
ATGCCTCCAT CGTGGnTGTC AGGGCGTATA AATTCATCTT GGGTCAAA GA TATTTGGTGT	120
GTACTT	126

(2) INFORMATION FOR SEQ ID NO: 4773:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:

GTCTTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT	60
GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAAGAn ACCTTGCGGT CTCAATGCGG	120
CTCATC	126

(2) INFORMATION FOR SEQ ID NO: 4774:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:

ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC 60
TGCATCTTnA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 120
TACG 124

(2) INFORMATION FOR SEQ ID NO: 4775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:

ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC 60
ACCAACACCA CCGACACCAG AAGTGCCGAG TGAnCCAGAA ACTCCAACAC CGCCAACACC 120
AGAG 124

(2) INFORMATION FOR SEQ ID NO: 4776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4776:

CCCGCTAGTC TCCACCATTT ATTTTTTACA CGATGAACAT TGAAAACThA ATACAATATG 60
CAACGTTAAT TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT 120
AATCAAACAT CATAA 135

(2) INFORMATION FOR SEQ ID NO: 4777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:

AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA 60
GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAACTG GACGCTGGAT GTGCGAAACG 120

TTGGGGGTTC AACAGGATT TAGA

144

(2) INFORMATION FOR SEQ ID NO: 4778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:

AATTTTGGAT GACGGGTCCC TTCCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG	60
TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCCT GTCTTCGACT GGCCTGCTC	120
CCT	123

(2) INFORMATION FOR SEQ ID NO: 4779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:

GCGCATTAAC TATCGCGATA TTAATCGCTA TTCTATATCG TCACTTTAGA GGATATCCTG	60
AACAATATAG CTCAGGTATT ACGTTTTTCAT CTAAATATTT ATTAAGATTT GCAATCATCC	120
TAnATGG	127

(2) INFORMATION FOR SEQ ID NO: 4780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:

GGTAATATGT TTAGCCCCGG TACATTTTCG GCGCAnTGTC CTCACTAGT GAGCTATTAC	60
GCACTCTTTA AATGATGGCT GCTTCTAAGC CAACATCCTA GTTGTCTGGG CAACGTCACA	120
TCCTTTT	127

(2) INFORMATION FOR SEQ ID NO: 4781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:

ACACnGGGTG AGAATTTGTC GCTATTTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT	60
GTCTTATTTT TTAAAGTAT TAAAAGTAA AATTACATGT TAATACGTAG TATTAAATGG	120
CGAGACTCC	129

(2) INFORMATION FOR SEQ ID NO: 4782:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:

CTCATTCCTG TTGCATTTTA TCTTCTGCAA CAACAACATT TCGTCTTTAT CGTCTTCCAT	60
AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTTCAT GTTTGnTTTG	120
GTCAGATTTA GGACCA	136

(2) INFORMATION FOR SEQ ID NO: 4783:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:

CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC	60
AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGGATT ATTGnGACGG TATTGTTGG	119

(2) INFORMATION FOR SEQ ID NO: 4784:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:

ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT	60
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nATCCCATG CATCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG 120
CGCACGG 127

(2) INFORMATION FOR SEQ ID NO: 4785:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:

ACACCGGCAT GCTGAATACT CGTTTTGGGT GAAGCCCCTG nACCACCATC GTAACCACTG 60
ATGACAATTT TATCTGCAA TGCTTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT 119

(2) INFORMATION FOR SEQ ID NO: 4786:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:

CTTTCTAAAC CCGnACCAC TTTATCGTGG TGGGGAGACA GTGTTcAGGC GGGCCAGTTT 60
GACTGGGGCC GGTCGCTCCT AAAAGTAACG AGGCGCTCAA AGTTCCTCA GAATGTTGGA 120
AATCATTCAT AGAGTGT 137

(2) INFORMATION FOR SEQ ID NO: 4787:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 basepairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:

GTTTTTAACA CTGTTACCGT TTTATCTTT TAATGTTACC GTTACGCCAG AnATACCTTT 60
TTATCTTGG TCTTGATAC CATTTTTATT TGTATCTTCC CAGACATAGT CACCTAAGT 119

(2) INFORMATION FOR SEQ ID NO: 4788:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:

CATGCTTCCA CCTCGAACCT ATTAACCTnC ATCATCTTTG AGGGATCTTA TAACCGCAGT	60
TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCCG	120
GCCACACATA GCTACCCAGC T	141

(2) INFORMATION FOR SEQ ID NO: 4789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:

CTGGGTTTCTAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGGCGTAA GAAATTTGAG	60
AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT	120
GCCAACGCAT AGCTGGGTA	139

(2) INFORMATION FOR SEQ ID NO: 4790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:

CATTATTTAG TATTTATGAG CTAATCAAAC AnCATAATTT TTATGGAGAG TTTGATCCTG	60
GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG	120
CTTGCTTCG	129

(2) INFORMATION FOR SEQ ID NO: 4791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:

GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT	60
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TATCAAAA_nC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC 120

(2) INFORMATION FOR SEQ ID NO: 4792:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:

CAAATTCTTT CGCTACTTGA ATGACAACAC TTTGTTTTAC GCCTGAAATG GCTTCTTGCC 60
AAGCAGGTGT ATATTTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC 120
CG_n 123

(2) INFORMATION FOR SEQ ID NO: 4793:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:

TTCTAAGATA TATTCGGAAC ATCTTCTTCA GAAATCGGAA TAACGTGACA TATTGTATTC 60
AGTTTTGAAT GTTTGTTTCA TCAAATTAAT GGGCCTATAG CTCAGTGGT TAGAGCGCAC 120
nCCTGATAAC 130

(2) INFORMATION FOR SEQ ID NO: 4794:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:

CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT 60
TAACTCATTT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGT_nGAAGGA CATCT 115

(2) INFORMATION FOR SEQ ID NO: 4795:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

nTTAAAAAAA ATTCCAATT TTTTTTGGGG GGTGGGAAT TTAAAAATTT GGTTTTTAAC	60
CCAAAGGCCC TTTTCCCAA AATTTAAATT CCCTTAAAAA TTAAAAATTT GGGAATTTTT	120
TTTTnGGCCC AAAATTTTTT CCCTTTTTTT AAAGGCCCCA ATTTTTAATT TAACCCTTAA	180
AACCCCAAAA CCTTTTTTCC TTTTTTAAAA TTTTTTTAAA TGGA	224

(2) INFORMATION FOR SEQ ID NO: 4796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:

TCGCGTACCG CTTTAATGGG CGAACAGCAA GACCTTGGGC ACCGACTACA GCCCCAnGAT	60
GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCGTCGAT GTGAACTCTT GGGGGCAGAT	120

(2) INFORMATION FOR SEQ ID NO: 4797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:

AATTCGATTC CCTTAGTAGC GGCGAGCGAA AGTGAAGAG CCCCAnACCA ACAAGCTTGG	60
CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC	120
ATCTG	125

(2) INFORMATION FOR SEQ ID NO: 4798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:

CAAAATAATG ACTCCTACGG GnCTCGAACC CGTGTTACCG CCGTGAAAGG GGGTGTCTT	60
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AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC 113

(2) INFORMATION FOR SEQ ID NO: 4799:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:

CCGGTGGGAG GTAACCTTTT AGGAGCTAGC CGTCGnAGGT GGGACAAATG ATTGGGGTGA 60
AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG 116

(2) INFORMATION FOR SEQ ID NO: 4800:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4800:

AGGACTTAAA AGCAGAATTA ATTGACCAAG TCGGTTACTT CATTGAGCCA GAAGATTTAT 60
TCAGTGCGAT GATTTCGTGAA ATTGAAACGC AAGATTTTCGA TATCGAnCAC CT 112

(2) INFORMATION FOR SEQ ID NO: 4801:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:

ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA 60
ATCCGGTACT CGTTAAGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC 110

(2) INFORMATION FOR SEQ ID NO: 4802:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:

GAACCAAGTT GTTATTGAAA AnTCGTTCGT AAAGTTACGG TACGCCCACC GTGAGTGCTT 60
 TTACTTCTAT ATCAGCACCT ACTGTATCTT TCATTAATTT AACGTCTTCT GCAGTCGCAC 120
 CGCCACCTGC AAAACCTGTT GAATTTTACG AGTCCGACC GCGCTTTGTA ATCATnCTTA 180
 CATTCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGCTCAGCGG AACACAA 237

(2) INFORMATION FOR SEQ ID NO: 4803:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:

CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA CCAATTGAGC TAAGCCGGGC 60
 AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTCGAA CCGCCGAnCC TCTG 114

(2) INFORMATION FOR SEQ ID NO: 4804:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 4804:

GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT 60
 GTTAGGGGTT TCCGCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT 113

(2) INFORMATION FOR SEQ ID NO: 4805:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC GCATCAGCGT CnGTTACAGA 60
 CCAGGAAAGT CGCCTTCGCC ACTGGTGTTT CTCCATATCT CTGCGCAT 108

(2) INFORMATION FOR SEQ ID NO: 4806:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:

TTTCAGCACT TATCCCGTCC ACACATAGTC TACCCAGGCT ATGCCGTTGG CACGACAACT 60
GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGAnAGCTC CTCTC 115

(2) INFORMATION FOR SEQ ID NO: 4807:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:

CAGCCACATA ACATAACTAA GTTTAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA 60
TGGTTAATAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT 120
TTCGTCTTAT GCACATTnTT CGCTGATGTC TGCAGAGTTT TTGTTGA 167

(2) INFORMATION FOR SEQ ID NO: 4808:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:

TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATGC TTGCAGCTAA ATTACCTTGC 60
ATCATTGCTA GCTTTTCTTG TATTAActGA TAnTTACTAA TTGGTTTGCC GAATTGCT 118

(2) INFORMATION FOR SEQ ID NO: 4809:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:

TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCGA TTGGAATTTc 60
TCCnATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCCGGTCC TCATCAtGG 120

TACCTGACTT CAACTGACCA GGGTAGACAC

150

(2) INFORMATION FOR SEQ ID NO: 4810:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

AAGAAGGCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCA_n 60

AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA 107

(2) INFORMATION FOR SEQ ID NO: 4811:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:

AGAGTG_nATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTCG AGGAAGACAC 60

AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTTCCA 117

(2) INFORMATION FOR SEQ ID NO: 4812:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:

CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGAT_nACTA AATCCGTCTT 60

TCGACCCTGC TCGACTTGTA AG_TCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA 120

ATG 123

(2) INFORMATION FOR SEQ ID NO: 4813:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

TAACCCGAGA GGGTCCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC 60

TAGCCCTAAA GCTATTTTCGG AGAGAACCAG CTATCTCCAG GTCGA 106

(2) INFORMATION FOR SEQ ID NO: 4814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:

CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG 60

GAATCGCGAA CGTTGGCCAA CTGCCAACGA TTGGCGTGGG AATCATCCAG TG 112

(2) INFORMATION FOR SEQ ID NO: 4815:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:

ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GGCGGCGGTT GAACCCGTCA TTCTGACA 60

TTTATTCTTA CATATTGCCG GnCTAGCTCA ATTGGTAGAG CAACTGACCT TGTAATCAGT 120

AGGTT 125

(2) INFORMATION FOR SEQ ID NO: 4816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:

GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATT AATGAAGATG 60

CTGTTGCTTA CACTGAAGAC GTTTATGnTT TCTGGCGTCC AACT 104

(2) INFORMATION FOR SEQ ID NO: 4817:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:

GTCGGGTAAG TTCCGGCCCCG CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACGnGAG 60
ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG 117

(2) INFORMATION FOR SEQ ID NO: 4818:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:

CTAAGGAACC TTGTCTTGGA CTGTGCACA ATCGCTTTCT TCTTTCCTCT CCTTCGGCTC 60
TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATTC 120
A 121

(2) INFORMATION FOR SEQ ID NO: 4819:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:

TCAGTTCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA GTGGAATCG CTAGTAATCG 60
TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTnAAGA 118

(2) INFORMATION FOR SEQ ID NO: 4820:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

CAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTTTCGGAG 60

AGAACCAGCT ATCTnCAGGT TCGATTGGAA TTTCTCCGCT ACCC

104

(2) INFORMATION FOR SEQ ID NO: 4821:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:

TCGTAGTGGT TTCCAACCAA GTTTTTATAA GTCAAACGCT CACATACGGC TTCGTTTTCA	60
TTATTTTAAA TGCTCATTTA CATAGTnAAC TCGCTTTAAA ATAATTTAAC TCATGTCGCT	120
AACGTTTTCT TTTATAAAAG TTTAACGGTT TTATCTGTGG TGTCT	165

(2) INFORMATION FOR SEQ ID NO: 4822:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:

GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCGTGCC TAATACATGG CAATCGAGCG	60
AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCGGACG GGTGAGTAAC ACG	113

(2) INFORMATION FOR SEQ ID NO: 4823:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:

CCGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCTACC ATCGACGCTA AGAACCTTTC	60
TTTGAnTTGT GACAATCGCT TGCTTCTTTC CTCTTCTTCG GCTCTC	106

(2) INFORMATION FOR SEQ ID NO: 4824:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:

TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC	60
CGACCCGCAC GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACTAGAGn	108

(2) INFORMATION FOR SEQ ID NO: 4825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:

TCTAGTGACC GATAGTGAAC CAGTACCGTG AGGATAAGGT GAAAGCACC CCGGAAGTAG	60
nTGTAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGGTA ATGGGT	116

(2) INFORMATION FOR SEQ ID NO: 4826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:

ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTTA	60
ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA	120
ATCCTTGTAT TGC GTGTCAT AnAGTCTTTG CTCCTTGCAC	160

(2) INFORMATION FOR SEQ ID NO: 4827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:

CGCATTGAGA CCGCAAGCTC TTTTTTTTAT GTCTAAAACG TCAAAATAAA AAGTAAACAC	60
AAAGAAAATG GTTGGCCnAG TGAAAACGTT TGAATCTGAC GAAACGAGAA AGAGC	115

(2) INFORMATION FOR SEQ ID NO: 4828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:

CCAAAATAGC CTTCATAATC CAAAAACAGG CTCCTTTGAC TATAGATTTT CGTTTCTGGT 60
TCAGAAAGCT TTTGATTAACTTTAAAGTAT nCCCAATTAT AAT 103

(2) INFORMATION FOR SEQ ID NO: 4829:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4829:

GGACCGAACT GTCTCAGC GTCCTnAACC CATCTCGCGT ACCGCTTTAA TGGGCGAACA 60
GCCAACCCCTT GGGACCGACT ACAGCCCAT GATGCGATGA GCCGACATCG A 111

(2) INFORMATION FOR SEQ ID NO: 4830:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:

GTTGTTGGGG CCCCGCCGGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT 60
TTTCGTTTCAG TCAACnACTG CCAATATAAC TTTGTAGAGC ATTGA 105

(2) INFORMATION FOR SEQ ID NO: 4831:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:

ACATTGAGTC TTCGAGTCGT TGCATTTAC ACTGCCGnGA AAGCCTCTA GATAGAAAAT 60
AGGTGCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA 102

(2) INFORMATION FOR SEQ ID NO: 4832:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:

TTnTAGAATG AACCGGCGAG TTACGATTG ATGCAAGGTT AAGCAGTAAA TGTGGAGCCG 60
TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTGCT CGTAGCC 107

(2) INFORMATION FOR SEQ ID NO: 4833:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:

TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAACCA GTGACTGTTG ACCTTGTTGT 60
CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTTGTTG ACGTGCTTnA 120
TTTTCAGCAT CAATTTGATC AATC 144

(2) INFORMATION FOR SEQ ID NO: 4834:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:

GGCTCAGATG nACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA 60
GCTTGCTTCT CTGGATGTTA GCGGCGGACG GGTGTAGTAA CACGTGGG 108

(2) INFORMATION FOR SEQ ID NO: 4835:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:

GACAAATGGTA GGnGAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG 60
 CTTAGAAGTG AGAATGCCGG TGTGAGTAC GAAAGACGCA GT 102

(2) INFORMATION FOR SEQ ID NO: 4836:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:

TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACTTTATGG GATTnGnCTT GACCTCGCGG 60
 TTTCGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCCAA 109

(2) INFORMATION FOR SEQ ID NO: 4837:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:

CTCCACGTAA GCTAGCGCTC ACGTTTCAA GGCTCCTACC TACCTGGTA CAAGCTGTGC 60
 CGGAATTTCA ATTTGCAngC TACAGTAAAG CTCCACGGGG GTC 103

(2) INFORMATION FOR SEQ ID NO: 4838:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

TCAAACACTC nCATACTGCT TTATTTTCAT AAACAATATC ACTTTAACCA AAAAATATTT 60
 GAATGTTAAA TAAACATTCA AACTGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG 120
 A 121

(2) INFORMATION FOR SEQ ID NO: 4839:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:

AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT	60
ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAn AAAG	104

(2) INFORMATION FOR SEQ ID NO: 4840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4840:

CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGGTA GGTAGGAGCC	60
TTGAAACGTG AGCGCTATTA GTGnAGGCGT GGTGGGTACT ACCCTAGCTG TGTTGGCTTT	120
CTAACCC	127

(2) INFORMATION FOR SEQ ID NO: 4841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:

CATCCCACCC CGGGCAAGGT TGACTAGmT TGGAAAAAAA CTTGGTTACA ACGTTATTTT	60
CATTCACTCA ACTACTGCCA ATATAATATT GnAAACTATA GGACATTTAT TAGTGTTC	120
CTTCT	125

(2) INFORMATION FOR SEQ ID NO: 4842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:

TGGTACGGCA TCTCACCCGT CTTTCGCTAC TCACACCGGC ATTCTCAmT CTAnGCGCTC	60
CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC	108

(2) INFORMATION FOR SEQ ID NO: 4843:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:

TAATGAAGGT CTTCGGATCG TAAAACTCTG TTATTAAGnA GGAACATGTG TGTAAGTAGC 60
TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT 108

(2) INFORMATION FOR SEQ ID NO: 4844:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:

CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGACCTGG GCAACGTTCT ACTCTAGCGG 60
AACCTAAGTT GGGCTACCAT CGACGnCTAA GAACCTTTCT TGACTIONGTGT ACAATCG 117

(2) INFORMATION FOR SEQ ID NO: 4845:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:

GACTGTTTAT CAAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG 60
CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA 108

(2) INFORMATION FOR SEQ ID NO: 4846:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:

CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTT ACTGGGACAC 60

AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATTnTGCC TGAAAAAGAC GCACAAGT 118

(2) INFORMATION FOR SEQ ID NO: 4847:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:

GATCCCCGGA CGGAGTGCTT AATGCGTAC TGACAGCACT AAGGGGCGGA AACCCCCTAA 60

CACnTAGCAC TCATCGTTTA CGGCGTGGAC TACCAGGGTA TCTA 104

(2) INFORMATION FOR SEQ ID NO: 4848:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:

CTGGCGATTA TGCTCTGTAA CGTGCTTTCC AATTTGGAAC GCACGTGnCC CTGCCCATAC 60

CTACGGGACT TGACTTATAT TGTTTGGCTT TGTACGTCAT TTCAACAA GACGCCCATG 120

CCAGCAACGC GATTACC 137

(2) INFORMATION FOR SEQ ID NO: 4849:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:

GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTA~~CT~~TACCG 60

TTTTGGCAGA CGGCACTTGG TGGTACTTTA GAAGTCAAAG ACAnGGGGGG GGGGGG 116

(2) INFORMATION FOR SEQ ID NO: 4850:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:

TCCTTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGnACCG	60
TTATAGTTAC GGTCCGCCGT TTA CTGGGGC TTCGATTCGT ATCTTCGCAG CTATATCTCA	120
CTCCT	125

(2) INFORMATION FOR SEQ ID NO: 4851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:

AAGTTGTATT TTAAAATAG TTCTTTAAAT TATATACCCA CCACATTTGG TGGGAGAACC	60
TAAAAAAAAG CACTTTCCCC AAAAATGGGA AAGTGC	96

(2) INFORMATION FOR SEQ ID NO: 4852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:

ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGnAT	60
GAACCGGCGA GTTCACGATT TAGATGCAAG GTTnAGCAG	100

(2) INFORMATION FOR SEQ ID NO: 4853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:

CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCCTGG TACCACCTAT AATCGTTTTTA	60
ATCGATGGGG GACCCATAGG ATAGCGAACC TGCGATTGGA T	101

(2) INFORMATION FOR SEQ ID NO: 4854:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:

GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACCAGAC GTGAGGAAAG 60
GTGAAAnACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT 102

(2) INFORMATION FOR SEQ ID NO: 4855:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:

ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA 60
CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG 104

(2) INFORMATION FOR SEQ ID NO: 4856:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:

CTACTGTCTT CATTCTTTCA GTTCTTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT 60
TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCCT CTnTGGTAAA TCGCTAACTC 120
CATCTCCTTA ACCCGGTA 138

(2) INFORMATION FOR SEQ ID NO: 4857:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:

TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA 60

TGGATGGCGC TATTGCTTTA GGTCATCCAT TAGGTGCTAC 100

(2) INFORMATION FOR SEQ ID NO: 4858:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:

CTTAACCTTG CAGCACCGTG CAGGCGTCAC CCTATACATC AnCTTACGGT TTAGCAGAGA 60
CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATCACTG CGGCTT 106

(2) INFORMATION FOR SEQ ID NO: 4859:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:

GTAACTCGCC GGTTCAATTCT ACAAAGGGC ACGCCAATCA CCCATTAACG GGCTCCTGAA 60
CTACTTGTTA AGCAACACGG TTTCCAGGGT TCTATTTCCA CTTCCCCTTT CCGGGGTnGC 120
TTTTTCAACC TTTTCCCCC TCCACGGTTA CT 152

(2) INFORMATION FOR SEQ ID NO: 4860:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:

GCCCGTACCG CAAACCGACA CAGGTAGTCA AGATGAnGAA TTCTAAGGTG AGCGAGCGAA 60
CTCTCGTTAA GGAACTCGGC AAACTGACCC CGTCACTTCG 100

(2) INFORMATION FOR SEQ ID NO: 4861:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:

CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA 60
AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT 104

(2) INFORMATION FOR SEQ ID NO: 4862:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60
CCTCCTGCGT GCAAAGCAGG CGCTCTG 87

(2) INFORMATION FOR SEQ ID NO: 4863:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:

ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAACT CTTTATTCAC TCGGTTTTGG 60
CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAnTTTTCA ATGTA 105

(2) INFORMATION FOR SEQ ID NO: 4864:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60
TGCCTTGCTG GATGATGCTA TGATATTGCA CATATGAAT CAACAGTGGT GCATGAACCT 120
GCAnTGGCT 129

(2) INFORMATION FOR SEQ ID NO: 4865:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:

AAACCGCAAG GTCAAGCAAA TCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC 60
TCGACTACnT GAAGCTGGAA ATCGCTATAA ATCGTAGATC 100

(2) INFORMATION FOR SEQ ID NO: 4866:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:

GTGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GnGGTATGCT 60
TATTTTTTAAT GGCATTGTGT ACGAGAGCAT TAGAGTTTGT ACTTGTGAGG TTATT 115

(2) INFORMATION FOR SEQ ID NO: 4867:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:

ACACCACTCC TCATTAACCT TCCAGACCG CAGCAGGCGT CACCCCTATA CATCACCTTA 60
CGGTTTAGCA GAGACCTGTG TTTTGTATAA 90

(2) INFORMATION FOR SEQ ID NO: 4868:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:

CACGAACGAT TGTCTTGCGT GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC 60
GCTACTGCTC ATCAGGGATT ACAAACC 87

(2) INFORMATION FOR SEQ ID NO: 4869:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4869:

GAGCACCCCT TCTCCCCAAG TTACGGGGTC ATTTTGCCGA GTTCCTTAAC GAGAGTCGCT	60
CGCTCACCTT AGAATCTATT TACTACTGGTG TTGGTAGGCA CTTTTTTCAA GCTTCCGATT	120
AACACATGAA AAGCTTCCAA AGTACTAGGA CGTTCAATAC ATGTA	165

(2) INFORMATION FOR SEQ ID NO: 4870:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:

AATATCATTT ATAACATTAA GTAATAACTT TTTTtAETT GTCCATTTTA TTTTtnAACC	60
AAAATTTGAT TAAAAAACTG CCTGGCAACG TTCTACTCTA GCGGAACTAA G	111

(2) INFORMATION FOR SEQ ID NO: 4871:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:

TAGCAGAGAC CTGTGTTTTT TGATAAACAG TCGCTTGGGC CTATTCCTG CGGCTCTTCT	60
GGGCGTTAAC CCTAAAGAGC ACCC	84

(2) INFORMATION FOR SEQ ID NO: 4872:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:

ACAGTAAAGC TCCACGGGTC TTTCCGTCCT GTCGCGGGTA ACTGCATCTT CACAGGTACT 60
 ATGATTTCAC CGATCTCTCn ATGAACAGTG CCAAATCGTA C 101

(2) INFORMATION FOR SEQ ID NO: 4873:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:

GACAGGCGTA GCGATGGAT AACAGTTGT ATTCCTGTAC CACCTATGAT CGTTTAAATC 60
 GATGGGGGGA AGCATAGGAT AGGCGAA 87

(2) INFORMATION FOR SEQ ID NO: 4874:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:

GGGAGAGCGC CTGCTTTGCA CGCAGGAGGT CAGCGGTTTCG ATCCCGCTAG TCTCCACCAT 60
 TATTTGTACA TTGAAACTA G 81

(2) INFORMATION FOR SEQ ID NO: 4875:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:

TATGTTTCGA AATATCTTTA TCACTCTAAA ATGATATACA AGAAATCCAA GAAAAATAAG 60
 CGAACTGAAT AAATAAGAT T 81

(2) INFORMATION FOR SEQ ID NO: 4876:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:

AACGCGTTAA ATCTTTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG 60
TGGAACATAG ATTAAGTTAT TAAGGGC 87

(2) INFORMATION FOR SEQ ID NO: 4877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:

ACAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA 60
CGGGGAGGTT TGnCTCAAT GTGGCTCATC GGATCTTGGG G 101

(2) INFORMATION FOR SEQ ID NO: 4878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:

ATTTATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AACAGCTCG CTAGGTCT 60
CAACTGCATG AGGTATATT 79

(2) INFORMATION FOR SEQ ID NO: 4879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:

ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAAGA 60
AAATTGGTAT GGTAATTGTG GCA 83

(2) INFORMATION FOR SEQ ID NO: 4880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:

CTTCATCCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA	60
TACTAAATAA TTTTGTA ACT AATA	84

(2) INFORMATION FOR SEQ ID NO: 4881:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:

TTGTGCAGTT GCATCGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTTCTG	60
CTTCACGCTT CTTCGCATTA	80

(2) INFORMATION FOR SEQ ID NO: 4882:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:

TCTGATGTGA AAGCCACGG CTCAACCGTG GAGGGTCATT GGAACTGGA AAAC TTGAGT	60
GCAGAAGAGG AAAGTGGGTT CCATGT	86

(2) INFORMATION FOR SEQ ID NO: 4883:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:

TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGACAAACAAGCTT CCATGACAAA	60
AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTTT GAAGGAACGT	120
CGGTTAA	127

(2) INFORMATION FOR SEQ ID NO: 4884:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:

AGTAGGAATC GAACCCACAC CAAAGTTTTG GAGACCTCTA TTCTACCTTG AACTATGCCC 60
CTATTAAAAA TAATAAAT 78

(2) INFORMATION FOR SEQ ID NO: 4885:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:

CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60
GTGGATTGTC CTTTGAAAT GGGT 84

(2) INFORMATION FOR SEQ ID NO: 4886:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:

GGTATCTGTT CACTCTCCG GTGGTGCACT TGCGACCAAC AATGGGTTGG AGATTGGATT 60
TCATCCTTCT CAATTAATCG TTGCCGTACT TTTCAANTGG TACCCCATCC AAAAGGG 117

(2) INFORMATION FOR SEQ ID NO: 4887:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:

CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCACT 60

ACCGTGAGGA AAGGTGAAAA

80

(2) INFORMATION FOR SEQ ID NO: 4888:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:

AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA 60

GGCCTTACGT TTGCGTG 77

(2) INFORMATION FOR SEQ ID NO: 4889:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:

TCTTCTGGGC GTTAACCCTA AAGAGCACCC CTTCTCCCGA GTTAGGGGT CTTTGGCCGA 60

GTTCCTTAAC GAGAGT 76

(2) INFORMATION FOR SEQ ID NO: 4890:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:

GTGGGGGCCC CAACATAGGA GCTGATTTTC TGTCAGCTTA CCATnATGTG GCAAGTTGGC 60

GGGGGGCCCC AAACCAAGGA GCTGGCTTTC TGTCACCTTA CCATTAATGT GGCAAGT 117

(2) INFORMATION FOR SEQ ID NO: 4891:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ IDNO: 4891:

TTAATCCnCC TGCATATGAT GACTTTGTTG AACCGTCATT GCATACTTTC AACATGAATA 60
CGCTGAACAC CTTCACTTAC TGCATATCTT AGTTCCTCGG TCTGTCTTA 109

(2) INFORMATION FOR SEQ ID NO: 4892:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG 60
AGACCGTGTG TTTTGTAGAA ACAGGTGC 88

(2) INFORMATION FOR SEQ ID NO: 4893:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTTCG GCAGTTCGAA 60
TCTGCCCCC TCCATTTATT ATTTTnAAAA AAAGCATAGT TC 102

(2) INFORMATION FOR SEQ ID NO: 4894:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTTC CGACTCAGAC AATGACTGG AATTCAGATA ACGAATCTGA CTCAGACAGT 60
GACTCAGATT CCGACAGT 78

(2) INFORMATION FOR SEQ ID NO: 4895:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

ACTAGATAGT AAGTAAAAGT GATTTTGCTT CCGAAACATT TATTTGATTA GTCTTCGTCG 60
TTAGTATTCG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTAC ACTTGGGGAC 120
TTATACCGAG TnGGAATCTC A 141

(2) INFORMATION FOR SEQ ID NO: 4896:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

GTTTCGGATTT AATTTGATTC ATTTGTTGCG TAATTTCAGA AGCCATTTTA TGAAAAGAGT 60
GATTTAATTC ATAAATTTCT 80

(2) INFORMATION FOR SEQ ID NO: 4897:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC 60
AAACCAATTA GTA 73

(2) INFORMATION FOR SEQ ID NO: 4898:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG 60
TGCGTCTGCC A 71

(2) INFORMATION FOR SEQ ID NO: 4899:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT	60
TAAGGCTGGA GCTGTnGATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGCG TGTTTT	116

(2) INFORMATION FOR SEQ ID NO: 4900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

TTCCGGCCCC TGGCGGTnTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC	60
CGGGCAGAGT CCCCTTCGAC TAAGAAAATC TCACATTCTT CAGGGACTTT TAC	113

(2) INFORMATION FOR SEQ ID NO: 4901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

ACTTAATGGA TTGATTAAGT AGTGGGTCTT TAACATTAGG CCTCAGCTAA TGTGGTACTT	60
AAAAATAGGG AATACATG	78

(2) INFORMATION FOR SEQ ID NO: 4902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT	60
CAAAACTAGA TAGTAAGTAA AAGT	84

(2) INFORMATION FOR SEQ ID NO: 4903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

TTGTCGGGTA AGTTCCGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG	05
AGACTCGGTG	70

(2) INFORMATION FOR SEQ ID NO: 4904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT	60
TCCTCTTCTT GGCTCTGCTT CTATTTGCCT CTAATGTGGC TTTTGTGTGT AATAAGTTAT	120
GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A	151

(2) INFORMATION FOR SEQ ID NO: 4905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

TGACTTGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC	60
TTATCGTGGT GGGGA	75

(2) INFORMATION FOR SEQ ID NO: 4906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

CGATTCGGAC TCAAGATAGC GGATTCAGGA TCACAGGC GAATCCAGAT CAGACCAGCG 60

ACTCAGACAG TGA CTCAGAT CAGATAGT G CTCGGATTCA GCGATTATTC AG 112

(2) INFORMATION FOR SEQ ID NO: 4907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGTACAC GTGCTACTAA 60

AGGTTTACCA 70

(2) INFORMATION FOR SEQ ID NO: 4908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

AGAAGATACA AATAAAGnTA AACCCAAATT ATTCAATTTT GGTGGGACAC AATAGTGTTG 60

ACTTTGAAGA AGATACTT TCCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC 120

C 121

(2) INFORMATION FOR SEQ ID NO: 4909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTCGTGA GATGTTGGGG 60

TTAAGTCCCCG 70

(2) INFORMATION FOR SEQ ID NO: 4910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 basepairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

GGACACCCGG AGAACTGAAA CATTTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG 60
TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG 100

(2) INFORMATION FOR SEQ ID NO: 4911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

nTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAATAAC 60
TTACTTATTC ATGATACACG CTTAATTAAT AAGGTGCAAT AGTTAATTTT AACTTTGAT 120
GTAAACTTTG GCACATCAGC TTTTAGTGTG TTTCG 155

(2) INFORMATION FOR SEQ ID NO: 4912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

CCCGTCACAC CACGAGATTT GTAACACCCG AAAGCCGGTG GAGTGAACCT TTTAGGAGCT 60
AGCCGTCGA 69

(2) INFORMATION FOR SEQ ID NO: 4913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTTA 60
GCGGAACGT 69

(2) INFORMATION FOR SEQ ID NO: 4914:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

CAAATGCTTC TGTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA 60
ATACTTCAT 69

(2) INFORMATION FOR SEQ ID NO: 4915:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

TATTTCCGGAG AGAACCAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT 60
CATCCGCTCA 70

(2) INFORMATION FOR SEQ ID NO: 4916:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTTCT ATTTCACTCC 60
CCTTCCG 67

(2) INFORMATION FOR SEQ ID NO: 4917:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:

TACTAAGACT GTGGACGCTA GAATGAGATG CCGTGTGATA GCGAAAACGG TGAGAATCCC 60

TCCACCGTTG ACTAAGGTTC CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120
 GGCGCACGTA GGCGATGATA CAGGTTATAT CCTnACACCT A 161

(2) INFORMATION FOR SEQ ID NO: 4918:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC 60
 ACATATGT 68

(2) INFORMATION FOR SEQ ID NO: 4919:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG 60
 AGTGACAATA CTTCAGGG 78

(2) INFORMATION FOR SEQ ID NO: 4920:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

AATTTGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTCGATTGC 60
 TACTTCGC 68

(2) INFORMATION FOR SEQ ID NO: 4921:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC	60
TTTACTG	67

(2) INFORMATION FOR SEQ ID NO: 4922:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT	60
GTCATG	66

(2) INFORMATION FOR SEQ ID NO: 4923:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA	60
TCGTGGGTGG GAG	73

(2) INFORMATION FOR SEQ ID NO: 4924:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTTATTT TTTACAGAT GACATGAAAC	60
TGATGACATA TGCACCGTAA TTCCAAAAA	89

(2) INFORMATION FOR SEQ ID NO: 4925:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

AATGGCATCG GAGTTGTCTG AATTCGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT 60
ACCTCCAA 66

(2) INFORMATION FOR SEQ ID NO: 4926:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

ACGAAAGGCG TAACGATTTG GGCACGTATC TCGACGAGAG ACTCGTGAAA ATCATAGATA 60
CCTGTGAAGA TGC 73

(2) INFORMATION FOR SEQ ID NO: 4927:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

ATTTCTATTA ATTATTTGCA TAGAAATCAG CTTTTTTGAT ATGTATTTTA TAATGTACAG 60
CTCGTTGAG 69

(2) INFORMATION FOR SEQ ID NO: 4928:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCCC 60
ACGACGTATA 70

(2) INFORMATION FOR SEQ ID NO: 4929:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG 60
GTGGGTCCCG ACACAGAGAA ATT 83

(2) INFORMATION FOR SEQ ID NO: 4930:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CTTGGTAGAG CACTTGGTTT GGGACCAAGG GGTCGCAGTT CGAATCCTGT CTTCCCGATT 60
ACTCTA 66

(2) INFORMATION FOR SEQ ID NO: 4931:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA 60
GACCG 65

(2) INFORMATION FOR SEQ ID NO: 4932:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4932:

TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GCGCATAGAT ATGGCAGGAA 60
CACCAGTGGG CGA 73

(2) INFORMATION FOR SEQ ID NO: 4933:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:

TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT 60
GTCTG 65

(2) INFORMATION FOR SEQ ID NO: 4934:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:

GAGCATGTGG GTTTAATTCG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCnT 60
TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTGCGGGGT AACAAATGTA CAGGTTGGTG 120

(2) INFORMATION FOR SEQ ID NO: 4935:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:

GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGGCGAT 60
GGATAACGGT TG 72

(2) INFORMATION FOR SEQ ID NO: 4936:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTT CTCCATATCT 60

CTGC

64

(2) INFORMATION FOR SEQ ID NO: 4937:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AATTCATGT 60
TGGT 64

(2) INFORMATION FOR SEQ ID NO: 4938:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60
GAT 63

(2) INFORMATION FOR SEQ ID NO: 4939:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

TAGAAATCAG CTTTTTTGCA TATGTATTTT ATAATGTACA GCTCGTTGAG CTGCTATTTT 60
CCT 63

(2) INFORMATION FOR SEQ ID NO: 4940:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT 60

TAGCTCAG 68

(2) INFORMATION FOR SEQ ID NO: 4941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTCG ATTCCCTTAG TAGCGGCGAG 60

CG 62

(2) INFORMATION FOR SEQ ID NO: 4942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

TTACAACAAT GCAATTGGCG GGGCCCAACA TAGAATGGC AATAGTTACT TTCAATAATG 60

TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

(2) INFORMATION FOR SEQ ID NO: 4943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTTAC AAACATTATT 60

TAGTATTGA 69

(2) INFORMATION FOR SEQ ID NO: 4944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT	60
GACGAATACG TAATTGA	77

(2) INFORMATION FOR SEQ ID NO: 4945:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 75 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTGAAGTT	60
CAGGTAACAC TGAAT	75

(2) INFORMATION FOR SEQ ID NO: 4946:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT	60
TCCCTATAGC GGCGnCGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG	120
TACAGCGCTG ACACT	135

(2) INFORMATION FOR SEQ ID NO: 4947:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

GATTTGGGCT CTTCCATTC GCTCGCCGCT ACTAAGGGAA TCGAATTTC TTTCTCTCC	60
T	61

(2) INFORMATION FOR SEQ ID NO: 4948:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

GCTTTTGAGG AATTTAATAT CAATATATAT TCTGTGTATGAAAATATTTT TCATAAAAAT 60
TGTTTGAATC 70

(2) INFORMATION FOR SEQ ID NO: 4949:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC 60
CTATTC 66

(2) INFORMATION FOR SEQ ID NO: 4950:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:

GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GTACGTTTT 60
TCACCGTAGG CATGCTGG 78

(2) INFORMATION FOR SEQ ID NO: 4951:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCGCGATAAT AAAAAATAAT GCGGAGGAA GAGGGATTCG AACCCCGTG GCCCGTTAAG 60
G 61

(2) INFORMATION FOR SEQ ID NO: 4952:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC 60
TGTAACCA 68

(2) INFORMATION FOR SEQ ID NO: 4953:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTGGGGAT CAAACAGGAT TAGATACCCT GGTAGTCCA 59

(2) INFORMATION FOR SEQ ID NO: 4954:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTGGCTTT 60

(2) INFORMATION FOR SEQ ID NO: 4955:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTGGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT 59

(2) INFORMATION FOR SEQ ID NO: 4956:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTCAGA TGAGAATTCT AAGGTGAGC 59

(2) INFORMATION FOR SEQ ID NO: 4957:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACACGTTTAG TTCACGCGGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT 60

TTTCAATGTA CAATTC 77

(2) INFORMATION FOR SEQ ID NO: 4958:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTCGTCAGC TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCTTAA 59

(2) INFORMATION FOR SEQ ID NO: 4959:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 59

(2) INFORMATION FOR SEQ ID NO: 4960:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAAGTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA 59

(2) INFORMATION FOR SEQ ID NO: 4961:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA 59

(2) INFORMATION FOR SEQ ID NO: 4962:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA 59

(2) INFORMATION FOR SEQ ID NO: 4963:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4963:

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGACTGCCGG TGACAAACCG 60

(2) INFORMATION FOR SEQ ID NO: 4964:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

TAGTTTTGGT ACGGTAACAA ATTTATTTGA AGAAACAATC TCAAATAAAG AATTGTTTG 59

(2) INFORMATION FOR SEQ ID NO: 4965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTTCGGTCC CTATCCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTACG 59

(2) INFORMATION FOR SEQ ID NO: 4966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTT TCAGTTCGG 59

(2) INFORMATION FOR SEQ ID NO: 4967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTTCGCT ATGTATATCG CATTAAACGT 60

TTGTC 65

(2) INFORMATION FOR SEQ ID NO: 4968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCCTCCGTTA CTTTTCAGAGG CGACGCCAG TCAAACGTCG CGCTGACACT GTCTCCCACC 60

(2) INFORMATION FOR SEQ ID NO: 4969:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCG 59

(2) INFORMATION FOR SEQ ID NO: 4970:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTACCG AGTCTCTCG TTGAGACAGT GCCCAAATCG 60
TTACG 65

(2) INFORMATION FOR SEQ ID NO: 4971:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGACTTGATG ACAATCGACT 60
TGCTTCTTTC CTCTCCTTCG GCTCTCACTT nCTCATTTAG 100

(2) INFORMATION FOR SEQ ID NO: 4972:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60

AGGTAGG

67

(2) INFORMATION FOR SEQ ID NO: 4973:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAATCATGC ATAAGAAATA CTAATTTC 58

(2) INFORMATION FOR SEQ ID NO: 4974:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA 58

(2) INFORMATION FOR SEQ ID NO: 4975:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GAGCCACAT CCTTTTCCAC TTGGCGTGTG TTTGGGACC TTGGCTGGTG GTCTGGGCTG 60

TTTCCCTA 68

(2) INFORMATION FOR SEQ ID NO: 4976:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTTCGA CCCTGACTCG ACTTGTAGGT CTCGCAGTCA AGCTCCCTT 59

(2) INFORMATION FOR SEQ ID NO: 4977:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTTAAAT 58

(2) INFORMATION FOR SEQ ID NO: 4978:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG 58

(2) INFORMATION FOR SEQ ID NO: 4979:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC 60

(2) INFORMATION FOR SEQ ID NO: 4980:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:

GTGGTGTGTT AGGGCACTCT ATACGGGTTA CAAAGTACGA CATTAGACGG ATCATCTGGA 60
AAGATGAATC AAAGT 75

(2) INFORMATION FOR SEQ ID NO: 4982:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

GTTTTTCATT TTCATTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA 58

(2) INFORMATION FOR SEQ ID NO: 4983:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCTGTAG 60
A 61

(2) INFORMATION FOR SEQ ID NO: 4984:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

GGTGTTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG 60
GAAA 64

(2) INFORMATION FOR SEQ ID NO: 4985:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCCAACAT AGAGAATTTC AAAAGAAAT 59

(2) INFORMATION FOR SEQ ID NO: 4986:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986

TGATGAAGGT CTTCGGATCG TAAAACTCTG TTATTAGGGA AGAACATATG TGTAAGT 57

(2) INFORMATION FOR SEQ ID NO: 4987:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

AAAGAATTTG CGCAAAACGC TATCGATACT GAAGGGCGTT CAATGATTAT CATGGGT 57

(2) INFORMATION FOR SEQ ID NO: 4988:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA 57

(2) INFORMATION FOR SEQ ID NO: 4989:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG 57

(2) INFORMATION FOR SEQ ID NO: 4990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT 60

G 61

(2) INFORMATION FOR SEQ ID NO: 4991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

TCCACGGGGT CTTTCCATCC TGTCTGGGT AACCTGCATC TTCACAGGTA CTATGATTTT 60

ACCGA 65

(2) INFORMATION FOR SEQ ID NO: 4992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCGGCTGG ATCACCTCCT TTCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT 57

(2) INFORMATION FOR SEQ ID NO: 4993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

CCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT T~~T~~ACTCTAG CGGAACG 57

(2) INFORMATION FOR SEQ ID NO: 4994:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGGTTTCGG GTCTACGACA AATACTAAAC GCCTATTCAG ACTCGCTTTC GCTACGG 57

(2) INFORMATION FOR SEQ ID NO: 4995:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

CAA~~A~~CTCTCG TGGTGTGACG GGCGGTGTGG TACAAGCCCC GGGAACGTAT TCACCGTAGC 60

ATGCCGGTCT ACG 73

(2) INFORMATION FOR SEQ ID NO: 4996:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

ACTAATTTCT ATAGGAAAAG TATTCTTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG 60

TAAGC 65

(2) INFORMATION FOR SEQ ID NO: 4997:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

ATTGGATTCC CAATTTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT 58

(2) INFORMATION FOR SEQ ID NO: 4998:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

AACTTCAACA GGTTTTGCAG GTGGCGGTGC GACTGCAGGA AGACGTTAAA TTAATG 56

(2) INFORMATION FOR SEQ ID NO: 4999:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTGT 56

(2) INFORMATION FOR SEQ ID NO: 5000:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC 56

(2) INFORMATION FOR SEQ ID NO: 5001:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC 56

(2) INFORMATION FOR SEQ ID NO: 5002:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

CCTGTCGGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG 56

(2) INFORMATION FOR SEQ ID NO: 5003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCA 56

(2) INFORMATION FOR SEQ ID NO: 5004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:

AATCCTTGTT TCGTTTTACG TCCGAGTGCG CCATTGTCAG ACAACGTATT TACAATT 57

(2) INFORMATION FOR SEQ ID NO: 5005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCAC TAGAA GCCGATG 57

(2) INFORMATION FOR SEQ ID NO: 5006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCAC TCCCCTG 57

(2) INFORMATION FOR SEQ ID NO: 5007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGAAGC TACAATTACG ATTGCAATCA 60

AACCAAAGA 69

(2) INFORMATION FOR SEQ ID NO: 5008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTC AGTCAACTAC TGCCAATATA ACTTCGT 57

(2) INFORMATION FOR SEQ ID NO: 5009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:

ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCAGC 56

(2) INFORMATION FOR SEQ ID NO: 5010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:

GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTTAC 60
TTGGG 65

(2) INFORMATION FOR SEQ ID NO: 5011:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:

TTTACTTGTA TTGGAATAAT TTCATCTTTG AACCGACCAT CACGTTGTGC GTCATA 56

(2) INFORMATION FOR SEQ ID NO: 5012:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:

CCTTATACAT CACCTTTACG GTTTTAGCAG AAACCTGTGT TTTTGTATAA ACAGTCGCTT 60

(2) INFORMATION FOR SEQ ID NO: 5013:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAAA TTGTGCAAGT TGGCGGGTCC 60

ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

TAGGGTAGTA TOCCACCAGT GGCCTCCACG TAAGCTAGCG CTTACGTTT CAAAGGCT 58

(2) INFORMATION FOR SEQ ID NO: 5015:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACTTGGGA nCAGACATGG GTGATAAGGT CGTGTTTCGAA 60

GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA 105

(2) INFORMATION FOR SEQ ID NO: 5016

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATTT ATTTATATGC TTATTTCTT ATTTATTATT ATTACAATTA CATTTT 56

(2) INFORMATION FOR SEQ ID NO: 5017:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

TCTGTAGAAA TTGGGGAATC CAATTTCTCT TGGTTTGGGT CCCATCCCCA ACTTGACAT 60

TATTG 65

(2) INFORMATION FOR SEQ ID NO: 5018:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

GGGGATGGGC CCCAACAAAG AGAAATTGGA TTCCAATTT CTAAGACAA TGCAAC 56

(2) INFORMATION FOR SEQ ID NO: 5019:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTC 55

(2) INFORMATION FOR SEQ ID NO: 5020:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

TACGGCGTTT AGTATTTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT 58

(2) INFORMATION FOR SEQ ID NO: 5021:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA 55

(2) INFORMATION FOR SEQ ID NO: 5022:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:

AGAGTTCACA TCGACGGGGA GGTTCGGCAC CTCGATGTCG GCTCATCGCA TCCTG 55

(2) INFORMATION FOR SEQ ID NO: 5023:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

CCTTAGCTGG TGGTCTGGGC TGTTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC 58

(2) INFORMATION FOR SEQ ID NO: 5024:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

TAAAGGCTAA ACTACCAATG TTTTCAATGG ATTTCCAAAA TGAATCATCT GGGAT 55

(2) INFORMATION FOR SEQ ID NO: 5025:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGGAATT 60

CCA 63

(2) INFORMATION FOR SEQ ID NO: 5026:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGC GTAC CTAAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT 60

AACG 64

(2) INFORMATION FOR SEQ ID NO: 5027:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA 56

(2) INFORMATION FOR SEQ ID NO: 5028:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

GGGCCCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT 55

(2) INFORMATION FOR SEQ ID NO: 5028:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:

CGTAACTATA ACGGTCCTAA GGTAGCGAA ATTCCTTGTC GGGTAAGTTC CGAC 54

(2) INFORMATION FOR SEQ ID NO: 5030:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:

ATCCCCGGGG CCCCAACACA GAGAATTTTCG AAAAGAAATT CTACAGGCAA TGCAAGT 57

(2) INFORMATION FOR SEQ ID NO: 5031:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:

TGCTTGGTAA AATCTATATT TTA~~CT~~TACTT ATCTAGTTTT CAATGTACAA TTTC 54

(2) INFORMATION FOR SEQ ID NO: 5032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGC~~T~~ TCCTTAGTAC GAGA 54

(2) INFORMATION FOR SEQ ID NO: 5033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:

AGAACACTCA CAAGATTAAT AACGCGTTTC CTGTAGGATG GAAACATAGA TTAA 54

(2) INFORMATION FOR SEQ ID NO: 5034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TATCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC 54

(2) INFORMATION FOR SEQ ID NO: 5035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGAAAAA 54

(2) INFORMATION FOR SEQ ID NO: 5036:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAAGAGC TTAAGTCTTG TGTTTCGGCAT GGGAACAGGT GTGA 54

(2) INFORMATION FOR SEQ ID NO: 5037:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG CGGAAG 56

(2) INFORMATION FOR SEQ ID NO: 5038:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

GACCGGGATG GACATACCTC TGGTGTACCA GTTTGTCGTG CCAACGCATA AGCT 54

(2) INFORMATION FOR SEQ ID NO: 5039:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTCACCGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG 54

(2) INFORMATION FOR SEQ ID NO: 5040:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

TTATAACACG TATGCTTGGG GAGTGTAAATA AGCTTGATCA GAGATTCCnA TGGGAACCAG 60

CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG 105

(2) INFORMATION FOR SEQ ID NO: 5041:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

GGCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC 54

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG 54

(2) INFORMATION FOR SEQ ID NO: 5043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 basepairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA 53

(2) INFORMATION FOR SEQ ID NO: 5044:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCCAGATT CCGACGGATT TCACGTGCT 59

(2) INFORMATION FOR SEQ ID NO: 5045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

TTTCGTCGTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG 60

TT 62

(2) INFORMATION FOR SEQ ID NO: 5046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

CGTCATCCCC ACCTTCCTCC GGTTTGTAC CAGTCAA CTTAGAGTGC CCA 53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG 53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

CCTCGGCACC ATTTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA 53

(2) INFORMATION FOR SEQ ID NO: 5049:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCCAA CTTAAGCCAG GATACAATTT ACAAATAGCG ACAATTCTC AATGTGTTT 59

(2) INFORMATION FOR SEQ ID NO: 5050:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5050:

CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAAGAC GTACTTCATG 60

TTACGTTGAC TTTAAGATGG TGGAACATAG TTAGTTTTAG GGCCACGGGG G 111

(2) INFORMATION FOR SEQ ID NO: 5051:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

ACGTTGACAT ATTGTCATTC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT 53

(2) INFORMATION FOR SEQ ID NO: 5052:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA 53

(2) INFORMATION FOR SEQ ID NO: 5053:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

AAATGCGGCT CATCGCATCC ATTTTTTGCC TGGCAACGTT CTACTCTAGC GGAC 54

(2) INFORMATION FOR SEQ ID NO: 5055:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTTGGACG AGG 53

(2) INFORMATION FOR SEQ ID NO: 5056:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTTCTTTT GCATAATTGA 60

CAA 63

(2) INFORMATION FOR SEQ ID NO: 5057:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCGCCAA CTTGCATTGT CTGTAGAATT CCTTTTCGAA ATTC

54

(2) INFORMATION FOR SEQ ID NO: 5058:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG

53

(2) INFORMATION FOR SEQ ID NO: 5059:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:

TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA

59

(2) INFORMATION FOR SEQ ID NO: 5060:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:

AAATAACTAA TAACATTTAG AGGCTGGAC ATAAATCCCT AAAAAACAGC AGT

53

(2) INFORMATION FOR SEQ ID NO: 5061:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:

TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC 55

(2) INFORMATION FOR SEQ ID NO: 5062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC ACATCAGCGT CA 52

(2) INFORMATION FOR SEQ ID NO: 5063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTCTTT GTGTTTCTTT TTATTTTAC GTTT TAGACA TA 52

(2) INFORMATION FOR SEQ ID NO: 5064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

CTCAAGCTCC CTTGTGCCTT TACTCTAT GTGTGCTTTC CGACCGTTCT GGGGGGA ACT 60

TTGGAGCGCC TCCGTT 76

(2) INFORMATION FOR SEQ ID NO: 5065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

CCACCGCTTG TCGGGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCGG TCGT 54

(2) INFORMATION FOR SEQ ID NO: 5066:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGGACAATG GTAGG 55

(2) INFORMATION FOR SEQ ID NO: 5067:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AA 52

(2) INFORMATION FOR SEQ ID NO: 5068:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA 60

GCGAGCGGAA ACAACAACAA CG 82

(2) INFORMATION FOR SEQ ID NO: 5069:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTGCGTC TA 52

(2) INFORMATION FOR SEQ ID NO: 5070:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCCAT CACAGCTCAG CCTTAACGAG TA 52

(2) INFORMATION FOR SEQ ID NO: 5071:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GA 52

(2) INFORMATION FOR SEQ ID NO: 5072:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

CACTTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA 53

(2) INFORMATION FOR SEQ ID NO: 5073:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTTCCG CAATGGGCGA AA 52

(2) INFORMATION FOR SEQ ID NO: 5074:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

TGTTGGCTTA GAATCAGCCA TCATTTAAAG AGTGC GTAAT AGCTCACTAG TCGC 54

(2) INFORMATION FOR SEQ ID NO: 5075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

AGAATTTTGA ATCCCGCGAC GATCTGCCAA TTCCGCCACA CCGGCTTAAT GGTAACA AAA 60

AAACTTCCCT TTGG 74

(2) INFORMATION FOR SEQ ID NO: 5076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

TGAGCTAATC AGACATCATA ATTTTATGG AGAGTTTAT CCTGGCTCAA GAT 53

(2) INFORMATION FOR SEQ ID NO: 5077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTAAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC CGCTAGAGTA GA 52

(2) INFORMATION FOR SEQ ID NO: 5078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTGGG CACTGTCTCA AC 52

(2) INFORMATION FOR SEQ ID NO: 5079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGGACC AGAAATGATG GTATTTAA~~Æ~~ AT 52

(2) INFORMATION FOR SEQ ID NO: 5080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:

AATAGCGACG AATCACACCT TCTGCGGCAC CACGGAATAA TACACCATGT GG 52

(2) INFORMATION FOR SEQ ID NO: 5081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:

CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA 52

(2) INFORMATION FOR SEQ ID NO: 5082:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:

CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA 56

(2) INFORMATION FOR SEQ ID NO: 5083:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:

AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTCCTA 60
CG 62

(2) INFORMATION FOR SEQ ID NO: 5084:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

GTGTACCAGT TGTCGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG 52

(2) INFORMATION FOR SEQ ID NO: 5085:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGGCAGATTC GAATGCGAAC 60
CCGAGGAGCG GATTAACA 78

(2) INFORMATION FOR SEQ ID NO: 5086:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT 52

(2) INFORMATION FOR SEQ ID NO: 5087:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

AAGTTGTTCT CAGTTCGGAT TGTA GTCTGC AACTCGACTA CATGAAGCTG G 51

(2) INFORMATION FOR SEQ ID NO: 5088:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

AATACTTTAA AAAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T 51

(2) INFORMATION FOR SEQ ID NO: 5089:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

AGAACGTAAA TTTAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G 51

(2) INFORMATION FOR SEQ ID NO: 5090:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCCT CAGTTCATCC GCTCACTTTT AACGTAAGT CCGTTCGGTC C 51

(2) INFORMATION FOR SEQ ID NO: 5091:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCA GACCACCAGC T 51

(2) INFORMATION FOR SEQ ID NO: 5092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:

TTGTGCGGAT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCC 55

(2) INFORMATION FOR SEQ ID NO: 5093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:

CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGACGAGCG A 51

(2) INFORMATION FOR SEQ ID NO: 5094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:

ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A 51

(2) INFORMATION FOR SEQ ID NO: 5095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:

AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT 60
ATTGTGCCAC CGATTGA 77

(2) INFORMATION FOR SEQ ID NO: 5096:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5096:

TTCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG 52

(2) INFORMATION FOR SEQ ID NO: 5097:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

GGGTCTGTTT TCTAATTGA GCACAATCTT CGTTCTCAAT AGAATGATTT A 51

(2) INFORMATION FOR SEQ ID NO: 5098:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCCAAC T 51

(2) INFORMATION FOR SEQ ID NO: 5099:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099

CTGTGGATTG TCCTTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A 51

(2) INFORMATION FOR SEQ ID NO: 5100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GGTTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A 51

(2) INFORMATION FOR SEQ ID NO: 5101:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTTCA ATTCTAGTCA GGGGCCCCAA 60

CACA 64

(2) INFORMATION FOR SEQ ID NO: 5102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAAGAA ACCTTGCGGT CTCAATGG 58

(2) INFORMATION FOR SEQ ID NO: 5103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATTT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 5104:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCCTCAGGAG TCTCGCATT AATACTACGT ATTAACATGT AAT

53

(2) INFORMATION FOR SEQ ID NO: 5105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

ATTTCTTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTTGT

50

(2) INFORMATION FOR SEQ ID NO: 5106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAC ACGGGTTCGA

50

(2) INFORMATION FOR SEQ ID NO: 5107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATAT ATGCGACAGT

50

(2) INFORMATION FOR SEQ ID NO: 5108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTTGTGT TTA CTTT TTA TTTTGACGTT TTAGACATAA 50

(2) INFORMATION FOR SEQ ID NO: 5109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTTACT AACGACGATA TGCTTTGGGG AGCTGTAAGT 50

(2) INFORMATION FOR SEQ ID NO: 5110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTCCGGTCTA 53

(2) INFORMATION FOR SEQ ID NO: 5111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCCGCCTGA GGAGTACGAC CTC 53

(2) INFORMATION FOR SEQ ID NO: 5112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT 50

(2) INFORMATION FOR SEQ ID NO: 5113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5113:

AGAnTTTCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCATTG 50

(2) INFORMATION FOR SEQ ID NO: 5114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTTGA TTTCACACTG 50

(2) INFORMATION FOR SEQ ID NO: 5115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAAAC TCATTATCAA GTTATGCACG TGTAATGAA TTCGGCTTTA TCGAA 55

(2) INFORMATION FOR SEQ ID NO: 5116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

GTA CTTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA 50

(2) INFORMATION FOR SEQ ID NO: 5117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTn

50

(2) INFORMATION FOR SEQ ID NO: 5118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:

CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA

50

(2) INFORMATION FOR SEQ ID NO: 5119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:

AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACTTTTAC TTACTATCTA

60

(2) INFORMATION FOR SEQ ID NO: 5120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:

CCGAAGTTTA OGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG

50

(2) INFORMATION FOR SEQ ID NO: 5121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:
ATAATCCTGT AGTCGAAAT GTTGTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG 60
T 61

(2) INFORMATION FOR SEQ ID NO: 5122

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:
TAGCGACTCA GATTGAGACA GCGATTCAGA CAGCGACTCA GACTCAGATA 50

(2) INFORMATION FOR SEQ ID NO: 5123:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:
TATTTGTAAA TTGTATCCTG GCTTAAGTTG GCCATTTTTC ATATGGTCTT 50

(2) INFORMATION FOR SEQ ID NO: 5124:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:
CACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCCGAGAAG GTCTCTATCT 60

(2) INFORMATION FOR SEQ ID NO: 5125:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

AGAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGCCGTAGTAAAA GCCTCTAGAT 60
AGAA 64

(2) INFORMATION FOR SEQ ID NO: 5126:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT 57

(2) INFORMATION FOR SEQ ID NO: 5127:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAGTTG 50

(2) INFORMATION FOR SEQ ID NO: 5128:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:

GCCGATTTTA GCAGTTGTTG CTCGTTCAA TTTTATGGGG CCATTTATGG 50

(2) INFORMATION FOR SEQ ID NO: 5129:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A 51

(2) INFORMATION FOR SEQ ID NO: 5130:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:

CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGGTCAA GGGTCGAATC CTCTTTT 57

(2) INFORMATION FOR SEQ ID NO: 5131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:

TGATATTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A 51

(2) INFORMATION FOR SEQ ID NO: 5132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:

TCCTGTAGTC GAACGTGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG A 51

(2) INFORMATION FOR SEQ ID NO: 5133:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:

ACTCAGACAT TGGATTGAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC 59

(2) INFORMATION FOR SEQ ID NO: 5134:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:

CCACCCCAAC GTTGCATTGT CTGTAGAAAT TGGGAATCCA ATTTCTCTTT

50

(2) INFORMATION FOR SEQ ID NO: 5135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATACnAAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG

50

(2) INFORMATION FOR SEQ ID NO: 5136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT

50

(2) INFORMATION FOR SEQ ID NO: 5138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGCTCCAC 50

(2) INFORMATION FOR SEQ ID NO: 5139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

GGTTCGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTGC TC 52

(2) INFORMATION FOR SEQ ID NO: 5140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT 56

(2) INFORMATION FOR SEQ ID NO: 5141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA 52

(2) INFORMATION FOR SEQ ID NO: 5142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT 56

(2) INFORMATION FOR SEQ ID NO: 5143:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAC AATTACATC CAAACCTTCA TCACTCACGC GCGTTGCTC CGTCAGCTTT 60
CGCCATTGCG AAGAT 75

(2) INFORMATION FOR SEQ ID NO: 5144:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55

(2) INFORMATION FOR SEQ ID NO: 5145:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53

(2) INFORMATION FOR SEQ ID NO: 5146:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T 51

(2) INFORMATION FOR SEQ ID NO: 5147:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA

50

(2) INFORMATION FOR SEQ ID NO: 5148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAATTC TCCAAAATAA TGA CTCCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 5149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAACTG AAACATCTTA AGTACCCGGA GAAAGAGAAA

50

(2) INFORMATION FOR SEQ ID NO: 5150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTTCGC ACTACCATCG ACGCTAAGGG AGCTTAACTT CTGTGGTTCG GCATGG

56

(2) INFORMATION FOR SEQ ID NO: 5151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

GGACTACCTG TGTCGAGTTT GCGGTAGGGG TCACCTGATT TTCTATCTAG AGGCTC 56

(2) INFORMATION FOR SEQ ID NO: 5152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTCGGGCTC ACCCCAATT GCACACTATT GTAAGCTGAC TTTCTCCA 59

(2) INFORMATION FOR SEQ ID NO: 5153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

TAACCACATC ATTCGATAC TGTTCATGGA AGTAATTTCT CTATTCTTCG GACCAGGAAA 60

ATACA 65

(2) INFORMATION FOR SEQ ID NO: 5154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

CCATATGTGT CAGTCACTGT GCAATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC 60

TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G 91

(2) INFORMATION FOR SEQ ID NO: 5155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

GGGAAAAGGA TGTGGTCGTT GCCCAGACAA CTAGGATGTT GGCTTATAAT CA

52

(2) INFORMATION FOR SEQ ID NO: 5156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCTCGTGACCGAT AGTGAACC

58

(2) INFORMATION FOR SEQ ID NO: 5157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAACTCC GGTATAGGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT G

51

(2) INFORMATION FOR SEQ ID NO: 5158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC

50

(2) INFORMATION FOR SEQ ID NO: 5159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T

51

(2) INFORMATION FOR SEQ ID NO: 5160:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

AACTGGAGAA ACAACTTTAT GGGGTTTGCT TGAACCTCGC GGTTTCGCTG CCCTTTGTAT 60
T 61

(2) INFORMATION FOR SEQ ID NO: 5161:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

AGACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T 51

(2) INFORMATION FOR SEQ ID NO: 5162:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

CCGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT 55

(2) INFORMATION FOR SEQ ID NO: 5163:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

CTTGATCTGT ATTTAAAATG ATATTTTCTA TCTTTTCTTT ATTATTAAACG TCTATGACGT 60
CGTAGTATAA GATTCCGTGT A 81

(2) INFORMATION FOR SEQ ID NO: 5164:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

GTTCGAATCC GTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC 60
AG 62

(2) INFORMATION FOR SEQ ID NO: 5165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

CAGGGGTCTT TCGTCCTGTG TGGGTAAGT CATCTTCACA GGTACTATGA TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 5166

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

AAGCTGAGGC CGACAGCGTA GGCGATGAT GACAGGTGA TATTGCCGGT ACCACCCGAT 60
AA 62

(2) INFORMATION FOR SEQ ID NO: 5167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

CTTGCGTCTC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CG 52

(2) INFORMATION FOR SEQ ID NO: 5168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

TCGTCCGCTA TCTCCACCAT TATTTGTACA TTGAACTAG ATA~~A~~TAGTA AATATA

56

(2) INFORMATION FOR SEQ ID NO: 5169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTTGGACGTC GGTGGGTAGT CGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCA

55

(2) INFORMATION FOR SEQ ID NO: 5170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

CTACTGCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCA TA

52

(2) INFORMATION FOR SEQ ID NO: 5171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAAGTTC TnAGGCAATG TAAAAAAGCT GATTCTATT

50

(2) INFORMATION FOR SEQ ID NO: 5172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 5172:

AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCAT TG CCATTCGAAG 60

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTTATTTT TTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn 50

(2) INFORMATION FOR SEQ ID NO: 5174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

CAACTCTCGT TAAGGAACTC GGCAAATAC CCCGTAAGT CGGAGTAGGT CTCTTTA 57

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA 60

(2) INFORMATION FOR SEQ ID NO: 5176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5176:

GTAACGGACG CGCTCAAAGG TTCCCTCACA ATGGTTGGAA ATCATT CATA 50

(2) INFORMATION FOR SEQ ID NO: 5177:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

AGTTACGTTC TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG 50

(2) INFORMATION FOR SEQ ID NO: 5178:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATTCCTG CGGCAATCTG GGG 53

(2) INFORMATION FOR SEQ ID NO: 5179:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

CGGTAACTTC ATACCTTTTA ACATATTTTG CATTTGATTG CGTTTACCTT TTTTACCTTT 60

ACCGCCACCA GTGAACTGTT TCA 83

(2) INFORMATION FOR SEQ ID NO: 5180:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:

TTAAACCCTT TTAATTGTTT GCCAGAACA CCATCGCTAT GGATGAAATT TAAAAAGCCG 60

TTTAAA 66

(2) INFORMATION FOR SEQ ID NO: 5181:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

GTTCGGTAAC TCGAGCGGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC 60
 GCAATAT 67

(2) INFORMATION FOR SEQ ID NO: 5182:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCAGTAG CGAAGGCAAC TTTCT 55

(2) INFORMATION FOR SEQ ID NO: 5183:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGnAC GAACACCAAT 50

(2) INFORMATION FOR SEQ ID NO: 5184:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

GAATCAGAGT TGGGGTGTGG GCCCGACGAA AGAGAAATTG GATTCCCGAA TTTCACGAG 60
 CC 62

(2) INFORMATION FOR SEQ ID NO: 5185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGT 55

(2) INFORMATION FOR SEQ ID NO: 5186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

CCATCATTA GTTGGGCACT CTAAGTTGAC TGCCGnGnC ACCnAAGAAG 50

(2) INFORMATION FOR SEQ ID NO: 5187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187

TTAATACGTT GCAATCCAAT CGCAGCTTC GCCTATCCTA CTGCCnTCCC 50

(2) INFORMATION FOR SEQ ID NO: 5188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTnAGTC GCTAnnCCAG 50

(2) INFORMATION FOR SEQ ID NO: 5189:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

ATAGATGCCC TTACCGCAAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT

54

(2) INFORMATION FOR SEQ ID NO: 5190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

CTTTAATGGG CGAACAGnAC CCTTGGACCG ACTACAGCCC AGATCGATGA

50

(2) INFORMATION FOR SEQ ID NO: 5191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT

60

(2) INFORMATION FOR SEQ ID NO:5192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu
1 5 10 15

Leu Leu Gly Ala Cys Gly Ala Ser Ala Thr Asp Ser Lys Glu Asn Thr
20 25 30

Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Va Ala Asp Thr Met Lys
35 40 45

Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu
50 55 60

Asn	Lys	Ile	Leu	Ala	Asp	Lys	Tyr	Lys	Asn	Lys	Val	Asn	Asp	Lys	Lys	
65					70					75					80	
Ile	Asp	Glu	Gln	Ile	Glu	Lys	Met	Gln	Lys	Gln	Tyr	Gly	Gly	Lys	Asp	
				85					90					95		
Lys	Phe	Glu	Lys	Ala	Leu	Gln	Gln	Gln	Gly	Leu	Thr	Ala	Asp	Lys	Tyr	
			100					105					110			
Lys	Glu	Asn	Leu	Arg	Thr	Ala	Ala	Tyr	His	Lys	Glu	Leu	Leu	Ser	Asp	
		115					120					125				
Lys	Ile	Lys	Ile	Ser	Asp	Ser	Glu	Ile	Lys	Glu	Asp	Ser	Lys	Lys	Ala	
	130					135					140					
Ser	His	Ile	Leu	Ile	Lys	Val	Lys	Ser	Lys	Lys	Ser	Asp	Xaa	Glu	Gly	
145					150					155					160	
Leu	Asp	Asp	Lys	Glu	Ala	Lys	Gln	Lys	Ala	Glu	Glu	Ile	Gln	Lys	Glu	
				165					170					175		
Val	Ser	Lys	Asp	Pro	Ser	Lys	Phe	Gly	Glu	Ile	Ala	Lys	Asp	Glu	Ser	
			180					185						190		
Met	Asp	Thr	Gly	Ser	Ala	Lys	Lys	Asp	Gly	Glu	Leu	Gly	Tyr	Val	Leu	
	195						200					205				
Lys	Gly	Gln	Thr	Asp	Lys	Asp	Phe	Glu	Lys	Ala	Leu	Phe	Lys	Leu	Lys	
	210					215					220					
Asp	Gly	Glu	Val	Ser	Glu	Val	Val	Lys	Ser	Ser	Phe	Gly	Tyr	His	Ile	
225					230					235					240	
Ile	Lys	Ala	Asp	Lys	Pro	Thr	Asp	Phe	Asn	Ser	Glu	Lys	Gln	Ser	Leu	
				245					250					255		
Lys	Glu	Lys	Leu	Val	Asp	Gln	Lys	Val	Gln	Lys	Asn	Pro	Lys	Leu	Leu	
			260					265					270			
Thr	Asp	Ala	Tyr	Lys	Asp	Leu	Leu	Lys	Glu	Tyr	Asp	Val	Asp	Phe	Lys	
		275					280					285				
Asp	Arg	Asp	Ile	Lys	Ser	Val	Val	Glu	Asp	Lys	Ile	Leu	Asn	Pro	Glu	
	290					295					300					
Lys	Leu	Lys	Gln	Gly	Gly	Ala	Gln	Gly	Gly	Gln	Ser	Gly	Met	Ser	Gln	
305				310						315					320	

(2) INFORMATION FOR SEQ ID NO:5193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

Met	Asn	Lys	Val	Ile	Lys	Met	Leu	Val	Val	Thr	Leu	Ala	Phe	Leu	Leu		
1				5					10					15			
Val	Leu	Ala	Gly	Cys	Ser	Gly	Asn	Ser	Asn	Lys	Gln	Ser	Ser	Asp	Asn		
			20					25					30				
Lys	Asp	Lys	Glu	Thr	Thr	Ser	Ile	Lys	His	Ala	Met	Gly	Thr	Thr	Glu		
		35					40					45					
Ile	Lys	Gly	Lys	Pro	Lys	Arg	Val	Val	Thr	Leu	Tyr	Gln	Gly	Ala	Thr		
	50					55					60						
Asp	Val	Ala	Val	Ser	Leu	Gly	Val	Lys	Pro	Val	Gly	Ala	Val	Glu	Ser		
65					70					75					80		
Trp	Thr	Gln	Lys	Pro	Lys	Phe	Glu	Tyr	Ile	Lys	Asn	Asp	Leu	Lys	Asp		
				85					90					95			
Thr	Lys	Ile	Val	Gly	Gln	Glu	Pro	Ala	Pro	Asn	Leu	Glu	Glu	Ile	Ser		
			100					105					110				
Lys	Leu	Lys	Pro	Asp	Leu	Ile	Val	Ala	Ser	Lys	Val	Arg	Asn	Glu	Lys		
		115					120					125					
Val	Tyr	Asp	Gln	Leu	Ser	Lys	Ile	Ala	Pro	Thr	Val	Ser	Thr	Asp	Thr		
	130					135					140						
Val	Phe	Lys	Phe	Lys	Asp	Thr	Thr	Lys	Leu	Met	Gly	Lys	Ala	Leu	Gly		
145					150					155					160		
Lys	Glu	Lys	Glu	Ala	Glu	Asp	Leu	Leu	Lys	Lys	Tyr	Asp	Asp	Lys	Val		
				165					170					175			
Ala	Ala	Phe	Gln	Lys	Asp	Ala	Lys	Ala	Lys	Tyr	Lys	Asp	Ala	Trp	Pro		
			180					185						190			
Leu	Lys	Ala	Ser	Val	Val	Asn	Phe	Arg	Ala	Asp	His	Thr	Arg	Ile	Tyr		
		195					200					205					
Ala	Gly	Gly	Tyr	Ala	Gly	Glu	Ile	Leu	Asn	Asp	Leu	Gly	Phe	Lys	Arg		
	210					215					220						
Asn	Lys	Asp	Leu	Gln	Lys	Gln	Val	Asp	Asn	Gly	Lys	Asp	Ile	Ile	Gln		
225					230					235				240			
Leu	Thr	Ser	Lys	Glu	Ser	Ile	Pro	Leu	Met	Asn	Ala	Asp	His	Ile	Phe		
				245					250					255			
Val	Val	Lys	Ser	Asp	Pro	Asn	Ala	Lys	Asp	Ala	Ala	Leu	Val	Lys	Lys		
			260					265					270				
Thr	Glu	Ser	Glu	Trp	Thr	Ser	Ser	Lys	Glu	Trp	Lys	Asn	Leu	Asp	Ala		
		275					280						285				
Val	Lys	Asn	Asn	Gln	Val	Ser	Asp	Asp	Leu	Asp	Glu	Ile	Thr	Trp	Asn		
	290					295					300						

Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr
 305 310 315 320

Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys
 325 330

(2) INFORMATION FOR SEQ ID NO:5194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Leu Ile Ala Thr Ile
 1 5 10 15

Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly
 20 25 30

Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr
 35 40 45

Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe
 50 55 60

Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val
 65 70 75 80

Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val
 85 90 95

Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala
 100 105 110

Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly
 115 120 125

Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile
 130 135 140

Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn
 145 150 155 160

Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pro Val Pro Tyr Ile Asn
 165 170 175

Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala
 180 185 190

Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr
 195 200 205

Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu

210		215		220
Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp				
225		230		235
Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu				
	245		250	255
Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val				
	260		265	270
Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Thr Gly				
	275		280	285
Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn				
	290		295	300
Lys Asn Leu Arg Leu Xaa Ser His Lys Gln				
305		310		

(2) INFORMATION FOR SEQ ID NO:5195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala		
1	5	10
Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser		
	20	30
Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp		
	35	45
Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn		
	50	60
Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe		
65	70	75
Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile Ser		
	85	90
Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys		
	100	105
Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Val Ile Pro		
	115	120
Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Glu Ala Ala		
	130	135
		140

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys
 145 150 155 160
 Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala
 165 170 175
 Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn
 180 185 190
 Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile
 195 200 205
 Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile
 210 215 220
 Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile
 225 230 235 240
 Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp
 245 250 255
 Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys
 260 265 270
 Ala Ile Glu Thr Ser Leu Ala Lys
 275 280

(2) INFORMATION FOR SEQ ID NO:5196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val
 1 5 10 15
 Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys
 20 25 30
 Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys
 35 40 45
 Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Gu Leu Asp Ile Lys Thr
 50 55 60
 Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile
 65 70 75 80
 Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys
 85 90 95

Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro
 100 105 110
 Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys
 115 120 125
 Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe
 130 135 140
 Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val
 145 150 155 160
 Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp
 165 170 175
 Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr
 180 185 190
 Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile
 195 200 205
 Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala
 210 215 220
 Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln
 225 230 235 240
 Asp Asp Lys Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp
 245 250 255
 Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala
 260 265 270
 Lys

(2) INFORMATION FOR SEQ ID NO:5197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

Met Lys Lys Ile Lys Tyr Ile Leu Val Val Phe Val Leu Ser Leu Thr
 1 5 10 15
 Val Leu Ser Gly Cys Ser Leu Pro Gly Leu Gly Ser Lys Ser Thr Lys
 20 25 30
 Asn Asp Val Lys Ile Thr Ala Leu Ser Thr Ser Glu Ser Gln Ile Ile
 35 40 45
 Ser His Met Leu Arg Leu Leu Ile Glu His Asp Thr His Gly Lys Ile

50	55	60
Lys 65	Pro Thr Leu Val Asn 70	Asn Leu Gly Ser 75
Ala 85	Leu Ile Asn Gly Asp Ala Asn Ile 90	Ser Gly Val Arg Tyr Asn Gly 95
Thr 100	Asp Leu Thr Gly Ala Leu Lys 105	Glu Ala Pro Ile Lys Asn Pro Lys 110
Lys 115	Ala Met Ile Ala Thr Gln Gln 120	Gly Phe Lys Lys Lys Phe Asp Gln 125
Thr 130	Phe Phe Asp Ser Tyr Gly Phe Ala Asn Thr 135	Tyr Ala Phe Met Val 140
Thr 145	Lys Glu Thr Ala Lys Lys Tyr His Leu 150	Glu Thr Val Ser Asp Leu 160
Ala 165	Lys His Ser Lys Asp Leu Arg Leu 170	Gly Met Asp Ser Ser Trp Met 175
Asn 180	Arg Lys Gly Asp Gly Tyr Glu Gly Phe LysLys 185	Glu Tyr Gly Phe 190
Asp 195	Phe Gly Thr Val Arg Pro Met Gln Ile Gly Leu Val 200	Tyr Asp Ala 205
Leu 210	Asn Ser Glu Lys Leu Asp Val Ala Leu Gly Tyr Ser Thr Asp Gly 215	220
Arg 225	Ile Ala Ala Tyr Asp Leu Lys Val Leu Lys Asp Asp Lys Gln Phe 230	235 240
Phe 245	Pro Pro Tyr Ala Ala Ser Ala Val Ala Thr Asn Glu Leu Leu Arg 250	255
Gln 260	His Pro Glu Leu Lys Thr Thr Ile Asn Lys Leu Thr Gly Lys Ile 265	270
Ser 275	Thr Ser Glu Met Gln Arg Leu Asn Tyr Glu Ala Asp Gly Lys Gly 280	285
Lys 290	Glu Pro Ala Val Val Ala Glu Glu Phe Leu Lys Lys His His Tyr 295	300
Phe 305	Asp Lys Gln Lys Gly Gly His Lys 310	

(2) INFORMATION FOR SEQ ID NO:5198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 284 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
1 5 10 15
Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
20 25 30
Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln AlaThr Lys Ala Tyr
35 40 45
Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
50 55 60
Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
65 70 75 80
Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
85 90 95
Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
100 105 110
Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
115 120 125
Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
130 135 140
Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
145 150 155 160
Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
165 170 175
Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Ile
180 185 190
Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
195 200 205
Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
210 215 220
Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
225 230 235 240
Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
245 250 255
Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
260 265 270
Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
275 280

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

```

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
1          5          10          15
Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
20          25          30
Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
35          40          45
Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
50          55          60
Lys Phe Val Lys Ala Ile Glu Asn Asn AspMet Ala Gln Ala Lys Ala
65          70          75          80
Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
85          90          95
Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
100         105         110
Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
115         120         125
Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
130         135         140
Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
145         150         155         160
Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
165         170         175
Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile
180         185         190
Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
195         200         205
Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu LysLys Asp Lys
210         215         220
Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
225         230         235         240
Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
245         250         255
Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu

```


- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

```

Met Leu Lys Gly Cys Gly Gly CysLeu Ile Ser Phe Ile Leu Leu Ile
1           5           10           15

Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser
          20           25           30

Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn
          35           40           45

Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu
          50           55           60

Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn
          65           70           75           80

Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp
          85           90           95

Asp Ile Asn Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu
          100          105          110

Lys Asp Asp Leu Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser
          115          120          125

Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser
          130          135          140

Phe Ala Asn Cys Lys Gln Leu Arg Gln Val TyrPro Asn Gly Val Thr
          145          150          155          160

Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys
          165          170          175

Arg Ala Cys Glu Pro Asp Lys Tyr
          180

```

(2) INFORMATION FOR SEQ ID NO:5202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile
1 5 10 15
Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr
20 25 30
Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys
35 40 45
Asp Ile Phe Xaa Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu
50 55 60
Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu
65 70 75 80
Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser
85 90 95
Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser
100 105 110
Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu
115 120 125
Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu MetMet Asn
130 135 140
Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile
145 150 155 160
Glu Lys Leu Ser Tyr Gln Pro Gh Asn Lys Ile Asn Val Val Asp Val
165 170 175
Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile
180 185 190
Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys
195 200 205

(2) INFORMATION FOR SEQ ID NO:5203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Xaa Leu Ile Phe Leu Ser
1 5 10 15

Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr
 20 25 30
 Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu
 35 40 45
 Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr
 50 55 60
 Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
 65 70 75 80
 Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
 85 90 95
 Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
 100 105 110
 Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
 115 120 125
 Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
 130 135 140
 Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
 145 150 155 160
 Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
 165 170 175
 Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
 180 185 190
 Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
 195 200 205
 Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
 210 215 220
 Asn Lys Gly Tyr Pro Val Ser Ile Val Tyr Pro Ile Glu Gly Thr Met
 225 230 235 240
 Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro
 245 250 255
 Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln
 260 265 270
 Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile
 275 280

(2) INFORMATION FOR SEQ ID NO:5204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5204:

```

Met Lys Lys Phe Ile Gly Ser Val Leu Ala Thr Thr Leu Ile Leu Gly
1           5           10           15

Gly Cys Ser Thr Met Glu Asn Glu Ser Lys Lys Asp Thr Lys Thr Glu
          20           25           30

Thr Lys Ser Val Pro Glu Glu Met Glu Ala Ser Lys Tyr Val Gly Gln
          35           40           45

Gly Phe Gln Pro Pro Ala Glu Lys Asn Ala Ile Glu Phe Ala Lys Lys
          50           55           60

His Arg Lys Glu Phe Glu Lys Val Gly Glu Gln Phe Phe Lys Asp Asn
65           70           75           80

Phe Gly Leu Lys Val Lys Ala Thr Asn Val Val Gly Lys Asp Asp Gly
          85           90           95

Val Glu Val Tyr Val His Cys Glu Asp His Gly Ile Val Phe Asn Ala
          100          105          110

Ser Leu Pro Leu Tyr Lys Asp Ala Ile His Gln Lys Gly Ser Met Arg
          115          120          125

Ser Asn Asp Asn Gly Asp Asp Met Ser Met Met Val Gly Thr Val Leu
          130          135          140

Ser Gly Phe Glu Tyr Arg Ala Gln Lys Glu Lys Tyr Asp Asn Leu Tyr
145          150          155          160

Lys Phe Phe Lys Glu Asn Glu Lys Lys Tyr Gln Tyr Thr Gly Phe Thr
          165          170          175

Lys Glu Ala Ile Asn Lys Thr Gln Asn Val Gly Tyr Lys Asn Glu Tyr
          180          185          190

Phe Tyr Ile Thr Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr
          195          200          205

Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met
          210          215          220

Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val
225          230          235          240

Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val
          245          250          255

Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys
          260          265          270

Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn
          275          280          285

Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val

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290

295

300

His Ser Lys Asp Glu
305

(2) INFORMATION FOR SEQ ID NO:5205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

Met	Lys	Lys	Leu	Val	Ser	Ile	Val	Gly	Ala	Thr	Leu	Leu	Leu	Ala	Gly	1	5	10	15
Cys	Gly	Ser	Gln	Asn	Leu	Ala	Pro	Leu	Glu	Glu	Lys	Thr	Thr	Asp	Leu	20	25	30	
Arg	Glu	Asp	Asn	His	Gln	Leu	Lys	Leu	Asp	Ile	Gln	Glu	Leu	Asn	Gln	35	40	45	
Gln	Ile	Ser	Asp	Ser	Lys	Ser	Lys	Ile	Lys	Gly	Leu	Glu	Lys	Asp	Lys	50	55	60	
Glu	Asn	Ser	Lys	Lys	Thr	Ala	Ser	Asn	Asn	Thr	Lys	Ile	Lys	Leu	Met	65	70	75	80
Asn	Val	Thr	Ser	Thr	Tyr	Tyr	Asp	Lys	Val	Ala	Lys	Ala	Leu	Lys	Ser	85	90	95	
Tyr	Asn	Asp	Ile	Glu	Lys	Asp	Val	Ser	Lys	Asn	Lys	Gly	Asp	Lys	Asn	100	105	110	
Val	Gln	Ser	Lys	Leu	Asn	Gln	Ile	Ser	Asn	Asp	Ile	Gln	Ser	Ala	His	115	120	125	
Thr	Ser	Tyr	Lys	Asp	Ala	Ile	Asp	Gly	Leu	Ser	Leu	Ser	Asp	Asp	Asp	130	135	140	
Lys	Lys	Thr	Ser	Lys	Asn	Ile	Asp	Lys	Leu	Asn	Ser	Asp	Leu	Asn	His	145	150	155	160
Ala	Phe	Asp	Asp	Ile	Lys	Asn	Gly	Tyr	Gln	Asn	Lys	Asp	Lys	Lys	Gln	165	170	175	
Leu	Thr	Lys	Gly	Gln	Gln	Ala	Leu	Ser	Lys	Leu	Asn	Leu	Asn	Ala	Lys	180	185	190	
Ser																			

(2) INFORMATION FOR SEQ ID NO:5206:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

Met	Lys	Arg	Leu	Leu	Phe	Val	Met	Ile	Ala	Phe	Val	Phe	Ile	Leu	Ala	1	5	10	15
Ala	Cys	Gly	Asn	Asn	Ser	Ser	Lys	Asp	Lys	Glu	Ala	Ser	Lys	Asp	Ser	20	25	30	
Lys	Thr	Ile	Asn	Val	Gly	Thr	Glu	Gly	Thr	Tyr	Ala	Pro	Phe	Ser	Phe	35	40	45	
His	Asp	Lys	Asp	Gly	Lys	Leu	Thr	Gly	Tyr	Asp	Ile	Asp	Val	Ile	Lys	50	55	60	
Ala	Val	Ala	Lys	Glu	Glu	Gly	Leu	Lys	Leu	Lys	Phe	Asn	Glu	Thr	Ser	65	70	75	80
Trp	Asp	Ser	Met	Phe	Ala	Gly	Leu	Asp	Ala	Gly	Arg	Phe	Asp	Val	Ile	85	90	95	
Ala	Asn	Gln	Val	Gly	Ile	Asn	Pro	Asp	Arg	Glu	Lys	Lys	Tyr	Lys	Phe	100	105	110	
Ser	Lys	Pro	Tyr	Thr	Phe	Ser	Ser	Ala	Val	Leu	Val	Ile	Arg	Glu	Asn	115	120	125	
Glu	Lys	Asp	Ile	Lys	Asp	Phe	Asp	Asp	Val	Lys	Gly	Lys	Lys	Leu	Ala	130	135	140	
Gln	Thr	Phe	Thr	Ser	Asn	Tyr	Gly	Lys	Leu	Ala	Lys	Asp	Lys	Gly	Ala	145	150	155	160
Asp	Ile	Thr	Lys	Val	Asp	Gly	Phe	Asn	Gln	Ser	Met	Asp	Leu	Leu	Leu	165	170	175	
Ser	Lys	Arg	Val	Asp	Gly	Thr	Phe	Asn	Asp	Ser	Leu	Ser	Tyr	Leu	Asp	180	185	190	
Tyr	Lys	Lys	Gln	Lys	Pro	Asn	Ala	Lys	Ile	Lys	Ala	Ile	Lys	Gly	Asn	195	200	205	
Ala	Glu	Gln	Ser	Arg	Ser	Ala	Phe	Ala	Phe	Ser	Lys	Lys	Ala	Asp	Asp	210	215	220	
Glu	Thr	Val	Gln	Lys	Phe	Asn	Asp	Gly	Leu	Lys	Lys	Ile	Glu	Glu	Asn	225	230	235	240
Gly	Glu	Leu	Ala	Lys	Ile	Gly	Lys	Lys	Trp	Phe	Gly	Gln	Asp	Val	Ser	245	250	255	

Lys Ser Lys

(2) INFORMATION FOR SEQ ID NO:5207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

Met	Gly	Val	His	Ser	Met	Lys	Leu	Lys	Arg	Leu	Phe	Ala	Val	Val	Ile	
1				5					10					15		
Ala	Met	Leu	Leu	Val	Leu	Ala	Gly	Gln	Ser	Asn	Ser	Asn	Asp	Asn	Asn	
			20					25					30			
Glu	Ser	Lys	Lys	Asp	Asp	Ala	Asp	Asn	Gly	Lys	Lys	Gln	Glu	Ile	Gln	
		35					40					45				
Val	Ala	Ala	Ala	Ala	Ser	Leu	Thr	Asp	Val	Thr	Lys	Lys	Leu	Ala	Ser	
	50					55					60					
Glu	Phe	Lys	Lys	Glu	His	Lys	Asn	Ala	Asp	Ile	Lys	Phe	Asn	Tyr	Gly	
65					70					75					80	
Gly	Ser	Gly	Ala	Leu	Arg	Lys	Gln	Ile	Glu	Ser	Gly	Ala	Pro	Val	Asp	
			85						90					95		
Val	Phe	Met	Ser	Ala	Asn	Thr	Lys	Asp	Val	Asp	Ala	Leu	Lys	Asp	Lys	
			100					105					110			
Asn	Lys	Ala	His	Asp	Thr	Tyr	Lys	Tyr	Ala	Lys	Asn	Ser	Leu	Val	Leu	
		115					120					125				
Ile	Gly	Asp	Lys	Asp	Ser	Asn	Tyr	Thr	Ser	Val	Lys	Asp	Leu	Lys	Asp	
	130					135					140					
Asn	Asp	Lys	Leu	Ala	Leu	Gly	Glu	Val	Lys	Thr	Val	Pro	Ala	Gly	Lys	
145					150					155					160	
Tyr	Ala	Lys	Gln	Tyr	Leu	Asp	Asn	Asn	Asn	Leu	Phe	Lys	Glu	Val	Glu	
			165					170						175		
Ser	Xaa	Ile	Val	Tyr	Ala	Lys	Asp	Val	Lys	Gln	Val	Leu	Asn	Tyr	Val	
			180					185					190			
Xaa	Lys	Gly	Asn	Ala	Lys	Gln	Gly	Phe	Val	Tyr						
		195					200									

(2) INFORMATION FOR SEQ ID NO:5208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met	Lys	Lys	Trp	Gln	Phe	Val	Gly	Thr	Thr	Ala	Leu	Gly	Ala	Thr	Leu	1	5	10	15
Leu	Leu	Gly	Ala	Cys	Gly	Gly	Gly	Asn	Gly	Gly	Ser	Gly	Asn	Ser	Asp	20	25	30	
Leu	Lys	Gly	Glu	Ala	Lys	Gly	Asp	Gly	Ser	Ser	Thr	Val	Ala	Pro	Ile	35	40	45	
Val	Glu	Lys	Leu	Asn	Glu	Lys	Trp	Ala	Gln	Asp	His	Ser	Asp	Ala	Lys	50	55	60	
Ile	Ser	Ala	Gly	Gln	Ala	Gly	Thr	Gly	Ala	Gly	Phe	Gln	Lys	Phe	Ile	65	70	75	80
Ala	Gly	Asp	Ile	Asp	Phe	Ala	Asp	Ala	Ser	Arg	Pro	Ile	Lys	Asp	Glu	85	90	95	
Glu	Lys	Gln	Lys	Leu	Gln	Asp	Lys	Asn	Ile	Lys	Tyr	Lys	Glu	Phe	Lys	100	105	110	
Ile	Ala	Gln	Asp	Gly	Val	Thr	Val	Ala	Val	Asn	Lys	Glu	Asn	Asp	Phe	115	120	125	
Val	Asp	Glu	Leu	Asp	Lys	Gln	Gln	Leu	Lys	Ala	Ile	Tyr	Ser	Gly	Lys	130	135	140	
Ala	Lys	Thr	Trp	Lys	Asp	Val	Asn	Ser	Lys	Trp	Pro	Asp	Lys	Lys	Ile	145	150	155	160
Asn	Ala	Val	Ser	Pro	Asn	Ser	Ser	His	Gly	Thr	Tyr	Asp	Phe	Phe	Glu	165	170	175	
Asn	Glu	Val	Met	Asn	Lys	Glu	Asp	Ile	Lys	Ala	Glu	Lys	Asn	Ala	Asp	180	185	190	
Thr	Asn	Ala	Ile	Val	Ser	Ser	Val	Thr	Lys	Asn	Lys	Glu	Gly	Ile	Gly	195	200	205	
Tyr	Phe	Gly	Tyr	Asn	Phe	Tyr	Val	Gln	Asn	Lys	Asp	Lys	Leu	Lys	Glu	210	215	220	
Val	Lys	Ile	Lys	Asp	Glu	Asn	Gly	Lys	Ala	Thr	Glu	Pro	Thr	Lys	Lys	225	230	235	240
Thr	Ile	Gln	Asp	Asn	Ser	Tyr	Ala	Leu	Ser	Arg	Pro	Leu	Phe	Ile	Tyr	245	250	255	
Val	Asn	Glu	Lys	Ala	Leu	Lys	Asp	Asn	Lys	Val	Met	Ser	Glu	Phe	Ile	260	265	270	

Lys Phe Val Leu Glu Asp Lys Gly Lys Ala AlaGlu Glu Ala Gly Tyr
 275 280 285
 Val Ala Ala Pro Glu Lys Thr Tyr Lys Ser Gln Leu Asp Asp Leu Lys
 290 295 300
 Ala Phe Ile Asp Lys Asn Gln Lys Ser Asp Asp Lys Lys Ser Asp Asp
 305 310 315 320
 Lys Lys Ser Glu Asp Lys Lys
 325

(2) INFORMATION FOR SEQ ID NO:5209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5209:

Met Lys Arg Leu Ser Ile IleVal Ile Ile Gly Ile Phe Ile Ile Thr
 1 5 10 15
 Gly Cys Asp Trp Gln Arg Thr Ser Lys Glu Arg Ser Lys Asn Ala Gln
 20 25 30
 Asn Gln Gln Val Ile Lys Ile Gly Tyr Leu Pro Ile Thr His Ser Ala
 35 40 45
 Asn Leu Met Met Thr Lys Lys Leu Leu Ser Gln Tyr Asn His Pro Lys
 50 55 60
 Tyr Lys Leu Glu Leu Val Lys Phe Asn Asn Trp Pro Asp Leu Met Asp
 65 70 75 80
 Ala Leu Asn Ser Gly Arg Ile Asp Gly Ala Ser Thr Leu Ile Glu Leu
 85 90 95
 Ala Met Lys Ser Lys Gln Lys Gly Ser Asn Ile Lys Ala Val Ala Leu
 100 105 110
 Gly His His Glu Gly Asn Val Ile Met Gly Gln Lys Gly Met His Leu
 115 120 125
 Asn Glu Phe Asn Asn Asn Gly Asp Asp Tyr His Phe Gly Ile Pro His
 130 135 140
 Arg Tyr Ser Thr His Tyr Leu Leu Leu GluGlu Leu Arg Lys Gln Leu
 145 150 155 160
 Lys Ile Lys Pro Gly His Phe Ser Tyr His Glu Met Ser Pro Ala Glu
 165 170 175

Met Pro Ala Ala Leu Ser Glu His Arg Ile Thr Gly Tyr Ser Val Ala
 180 185 190
 Glu Pro Phe Gly Ala Leu Gly Glu Lys Leu Gly Lys Gly Lys Thr Leu
 195 200 205
 Lys His Gly Asp Asp Val Ile Pro Asp Ala Tyr Cys Cys Val Leu Val
 210 215 220
 Leu Arg Gly Glu Leu Leu Asp Gln His Lys Asp Val Ala Gln Ala Phe
 225 230 235 240
 Val Gln Asp Tyr Lys Lys Ser Gly Phe Lys Met Asn Asp Arg Lys Gln
 245 250 255
 Ser Val Asp Ile Met Thr His His Phe Lys Gln Ser Arg Asp Val Leu
 260 265 270
 Thr Gln Ser Ala Ala Trp Thr Ser Tyr Gly Asp Leu Thr Ile Lys Pro
 275 280 285
 Ser Gly Tyr Gln Glu Ile Thr Thr Leu Val Lys Gln His His Leu Phe
 290 295 300
 Asn Pro Pro Ala Tyr Asp Asp Phe Val Glu Pro Ser Leu Tyr Lys Glu
 305 310 315 320
 Ala Ser Arg Ser

(2) INFORMATION FOR SEQ ID NO:5210:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val
 1 5 10 15
 Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser
 20 25 30
 Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys
 35 40 45
 Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly
 50 55 60
 Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu
 65 70 75 80
 Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys

	85		90		95										
Glu	Leu	Met	Gly	Lys	Val	Glu	Leu	Ala	Asp	Tyr	Arg	Phe	Thr	Lys	Asp
			100					105					110		
Ser	Lys	Gly	Ser	Ser	Ile	Lys	Asp	Val	Asp	Ala	Phe	Phe	Lys	Gly	Lys
		115					120					125			
Lys	Gly	Ile	Lys	Arg	Lys	Val	Ile	Glu	Thr	His	Asp	Asp	Val	Lys	Gln
	130					135					140				
Val	Asp	Tyr	Trp												
145															

(2) INFORMATION FOR SEQ ID NO:5211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

Trp	Pro	Cys	Ala	Thr	Xaa	Gln	Glx	Glu	Trp	Trp	Ser	Arg	His	Xaa	Trp
1				5					10					15	
Cys	Val	Cys	Asx	Met	Val	Arg	Asn	Leu	Ile	Lys	Asp	Glx	Glu	Glu	Leu
			20				25						30		
His															

(2) INFORMATION FOR SEQ ID NO:5212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 490 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

Met	Ser	Ile	Ile	Met	Glu	Val	Ala	Thr	Met	Gln	Ala	Lys	Leu	Thr	Lys
1				5					10					15	
Asn	Glu	Phe	Ile	Glu	Trp	Leu	Lys	Thr	Ser	Glu	Gly	Lys	Gln	Phe	Asn
			20					25					30		
Val	Asp	Leu	Trp	Tyr	Gly	Phe	Gln	Cys	Phe	Asp	Tyr	Ala	Asn	Ala	Gly
		35					40					45			

Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
 50 55 60
 Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
 65 70 75 80
 Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
 85 90 95
 Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
 100 105 110
 Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
 115 120 125
 Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
 130 135 140
 Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
 145 150 155 160
 Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro
 165 170 175
 Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
 180 185 190
 Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn
 195 200 205
 Pro Lys Gly Ile Val Ile His Asn Asp Ala Gly Ser Lys Gly Ala Thr
 210 215 220
 Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg Leu
 225 230 235 240
 Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp Gln
 245 250 255
 Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile Gly
 260 265 270
 Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp
 275 280 285
 Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala
 290 295 300
 Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg
 305 310 315 320
 Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val
 325 330 335
 Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp
 340 345 350
 Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr
 355 360 365

Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser Ala
370 375 380

Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala Trp Lys Arg Asn Lys
385 390 395 400

Tyr Gly Thr Tyr Tyr Met Glu Glu Ser Ala Arg Phe Thr Asn Gly Asn
405 410 415

Gln Pro Ile Thr Val Arg Lys Val Gly Pro Phe Leu Ser Cys Pro Val
420 425 430

Gly Tyr Gln Phe Gln Pro Gly Gly Tyr Cys Asp Tyr Thr Glu Val Met
435 440 445

Leu Gln Asp Gly His Val Trp Val Gly Tyr Thr Trp Glu Gly Gln Arg
450 455 460

Tyr Tyr Leu Pro Ile Arg Thr Trp Asn Gly Ser Ala Pro Pø Asn Gln
465 470 475 480

Ile Leu Gly Asp Leu Trp Gly Glu Ile Ser
485 490

(2) INFORMATION FOR SEQ ID NO:5213:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

Gly Asp Lys Met Asn Lys Ile Ser Lys TyrIle Ala Ile Ala Ser Leu
1 5 10 15

Ser Val Ala Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala
20 25 30

Phe Ala Lys Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile
35 40 45

Pro Ala Ser Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val
50 55 60

Ala Trp Tyr Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly
65 70 75 80

Tyr Asn Ser Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys
85 90 95

Gly Lys His Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu
100 105 110

Asp Asn Ser Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe

115	120	125
Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val 130 135 140		
Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys LysGly Val Asp 145 150 155 160		
Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr 165 170 175		
Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His 180 185 190		
Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln 195 200 205		
Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu 210 215 220		
Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala 225 230 235 240		
Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe 245 250 255		
Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn 260 265 270		
Tyr Lys Ala Ser Xaa Lys Ala Lys Asp Lys Leu Arg Lys Asn Ala Ile 275 280 285		
Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys 290 295		

(2) INFORMATION FOR SEQ ID NO:5214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn 1 5 10 15
Lys Leu Ile Ala Lys Ser Leu Leu Thr LeuAla Ala Ile Gly Ile Thr 20 25 30
Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro 35 40 45
Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn 50 55 60

Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro
 65 70 75 80
 Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp
 85 90 95
 Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala
 100 105 110
 Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln
 115 120 125
 Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg
 130 135 140
 Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys
 145 150 155 160
 Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu LysGln Gly Leu
 165 170 175
 Val Lys

(2) INFORMATION FOR SEQ ID NO:5215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 173 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

Lys Glu Arg Val Leu Met Lys Lys Leu Leu Thr Ala Ser Ile Ile Ala
 1 5 10 15
 Cys Ser Val Val Met Gly Val Gly Leu Val Asn Thr Ser Ala Glu Ala
 20 25 30
 Ala Ser Gly Asn Ser Ile Asp Thr Val Lys Gln Leu Ile Lys Gly Asp
 35 40 45
 Gln Ser Leu Glu Asn Val Lys Ile Gly Glu Ser Ile Lys Asp Val Leu
 50 55 60
 Thr Lys Tyr Lys Asn Pro Met Tyr Ser Tyr Asn Glu Ap Gly Thr Glu
 65 70 75 80
 His Tyr Tyr Glu Phe His Thr Lys Lys Gly Met Leu Leu Val Thr Thr
 85 90 95
 Asp Gly Lys Lys Asn Asn Gly Lys Val Thr His Ile Ser Met Met Tyr
 100 105 110

Asn Asp Ala Asn Gly Pro Thr Tyr Gln Ala Val Lys Asn Tyr Val Gly
 115 120 125
 Lys Ala Val Thr His Thr Glu Tyr Ser Lys Val Ala Gly Asn Phe Gly
 130 135 140
 Tyr Ile Glu Lys Gly Lys Thr Thr Tyr Gln Phe Ala Ser Ala Pro Lys
 145 150 15 160
 Asp Lys Asn Ile Lys Leu Tyr Arg Ile Asp Leu Glu Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:5216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

Phe Glu Val Arg Glu Ser Met Ser Asn Gln Asn Tyr Asp Tyr Asn Lys
 1 5 10 15
 Asn Glu Asp Gly Ser Lys Lys Lys Met Ser Thr Thr Ala Lys Val Val
 20 25 30
 Ser Ile Ala Thr Val Leu Leu Leu Leu Gly Gly LeuVal Phe Ala Ile
 35 40 45
 Phe Ala Tyr Val Asp His Ser Asn Lys Ala Lys Glu Arg Met Leu Asn
 50 55 60
 Glu Gln Lys Gln Glu Gln Lys Glu Lys Arg Gln Lys Glu Asn Ala Glu
 65 70 75 80
 Lys Glu Arg Lys Lys Lys Lys Gln Gln Glu Glu Lys Glu Gln Asn Glu Leu
 85 90 95
 Asp Ser Gln Ala Asn Gln Tyr Gln Gln Leu Pro Gln Gln Asn Gln Tyr
 100 105 110
 Gln Tyr Val Pro Pro Gln Gln Gln Ala Pro Thr Lys Gln Arg Pro Ala
 115 120 125
 Lys Glu Glu Asn Asp Asp Lys Ala Ser Lys Asp Glu Ser Lys Asp Lys
 130 135 140
 Asp Asp Lys Ala Ser Gln Asp Lys Ser Asp Asp Asn Gln Lys Lys Thr
 145 150 155 160
 Asp Asp Asn Lys Lys Gln Pro Ala
 165

(2) INFORMATION FOR SEQ ID NO:5217:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:

```

Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser
1           5           10           15

Leu Ser Val Thr Pro Ile Ala Asn Ala Glu Ser Asn Ser Asn Ile Lys
          20           25           30

Ala Lys Asp Lys Lys His Val Gln Val Asn Val Glu Asp Lys Ser Val
          35           40           45

Pro Thr Asp Val Arg Asn Leu Ala Gln Lys Asp Tyr Leu Ser Tyr Val
          50           55           60

Thr Ser Leu Asp Lys Ile Tyr Asn Lys Glu LysAla Ser Tyr Thr Leu
65           70           75           80

Gly Glu Pro Phe Lys Ile Tyr Lys Phe Asn Lys Lys Ser Asp Gly Asn
          85           90           95

Tyr Tyr Phe Pro Val Leu Asn Thr Glu Gly Asn Ile Asp Tyr Ile Val
          100          105          110

Thr Ile Ser
          115

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(2) INFORMATION FOR SEQ ID NO:5218:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5218:

```

Asn Phe Lys Met Gln Glu Val Lys Tyr Met Thr Glu Ile Thr PheLys
1           5           10           15

Gly Gly Pro Ile His Leu Lys Gly Gln Gln Ile Asn Glu Gly Asp Phe
          20           25           30

Ala Pro Asp Phe Thr Val Leu Asp Asn Asp Leu Asn Gln Val Thr Leu
          35           40           45

```

Ala Asp Tyr Ala Gly Lys Lys Lys Leu Ile Ser Val Val Pro Ser Ile
50 55 60

Asp Thr Gly Val Cys Asp Gln Gln Thr Arg Lys Phe Asn Ser Asp Ala
65 70 75 80

Ser Lys Glu Glu Gly Ile Val Leu Thr Ile Ser Ala Asp Leu Pro Phe
85 90 95

Ala Gln Lys Arg Trp Cys Ala Ser Ala Gly Leu Asp Asn Val Ile Thr
100 105 110

Leu Ser Asp His Arg Asp Leu Ser Phe Gly Glu Asn Tyr Gly Val Val
115 120 125

Met Glu Glu Leu Arg Leu Leu Ala Arg Ala Val Phe Val Leu Asp Ala
130 135 140

Asp Asn Lys Val Val Tyr Lys Glu Ile Val Ser Glu Gly Thr Asp Phe
145 150 155 160

Pro Asp Phe Asp Ala Ala Leu Ala Ala Tyr Lys Asn Ile
165 170

(2) INFORMATION FOR SEQ ID NO:5219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

Ile Glu Ser Arg Phe Ile Met Ala Lys Ile Asn Phe Asp Ala Ala Thr
1 5 10 15

Lys Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val Ile Lys Glu Asp
20 25 30

Glu Gln His Tyr Thr Tyr Thr His Glu Leu Gly Glu Met Asp Asn His
35 40 45

Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu His Ala Arg Glu
50 55 60

Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser Lys Leu Ile Ala
65 70 75 80

Asp Ser Ile Glu Ala Gly Tyr Val Lys Asn Ala Asn Phe Lys Pro Tyr
85 90 95

Phe Asp Gln Ile Glu Ile Phe Glu Lys Asp Phe Asp Leu Leu Phe Val
100 105 110

Lys Trp Ile Pro Arg Glu Gln Asn Lys Glu Ala Asn Gln His Ala Gln
 115 120 125

Gln Ala Leu Tyr Lys Leu Ile Lys Lys Asn Lys
 130 135

(2) INFORMATION FOR SEQ ID NO:5220:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

Met Pro Gly Thr Val Leu Asp Pro Gln Met Ile Lys Asn Glu Asp Val
 1 5 10 15

Ser Glu Lys Glu Tyr Ala Ala Val Ser Gln Gln Leu Ser Lys Leu Pro
 20 25 30

Gly Val Asn Thr Ser Met Asp Trp Asp Arg Lys Tyr Pro Tyr Gly Asp
 35 40 45

Thr Leu Arg Gly Ile Phe Gly Asp Val Ser Thr Pro Ala Glu Gly Ile
 50 55 60

Pro Lys Glu Leu Thr Glu His Tyr Leu Ser Lys Gly Tyr Ser Arg Asn
 65 70 75 80

Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr Gln Tyr Glu Asp Val Leu
 85 90 95

Arg Gly Lys Lys Lys Glu Met Lys Tyr Thr Thr Asp Lys Ser Gly Lys
 100 105 110

Val Thr Ser Ser Glu Val Leu Xaa Pro Gly Ala Arg Gly Gln Asp Leu
 115 120 125

Lys Leu Thr Ile Asp Ile Asp Leu Gln Lys Glu Val Glu Ala Leu Leu
 130 135 140

Asp Lys Gln Ile Lys Lys Leu Ala Val Lys Val Pro Lys Ile Trp Ile
 145 150 155 160

Met Gln

(2) INFORMATION FOR SEQ ID NO:5221:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:

Ile	Met	Ala	Tyr	Asp	Gly	Leu	Phe	Thr	Lys	Lys	Met	Val	Glu	Ser	Leu	
1				5					10					15		
Gln	Phe	Leu	Thr	Thr	Gly	Arg	Val	His	Lys	Ile	Asn	Gln	Pro	Asp	Asn	
			20					25					30			
Asp	Thr	Ile	Leu	Met	Val	Val	Arg	Gln	Asn	Arg	Gln	Asn	His	Gln	Leu	
		35					40					45				
Leu	Leu	Ser	Ile	His	Pro	Asn	Phe	Ser	Arg	Leu	Gln	Leu	Thr	Thr	Lys	
	50					55					60					
Lys	Tyr	Asp	Asn	Pro	Phe	Asn	Pro	Pro	Met	Phe	Ala	Arg	Val	Phe	Arg	
65					70					75					80	
Lys	His	Leu	Glu	Gly	Gly	Ile	Ile	Glu	Ser	Ile	Lys	Gln	Ile	Gly	Asn	
			85					90						95		
Asp	Arg	Arg	Ile	Glu	Ile	Asp	Ile	Lys	Ser	Lys	Asp	Glu	Ile	Gly	Asp	
			100					105					110			
Thr	Ile	Tyr	Arg	Thr	Val	Ile	Leu	Glu	Ile	Met	Gly	Lys	His	Ser	Asn	
		115					120					125				
Leu	Ile	Leu	Val	Asp	Glu	Asn	Arg	Lys	Ile	Ile	Glu	Gly	Phe	Lys	His	
	130					135					140					
Leu	Thr	Pro	Asn	Thr	Asn	His	Tyr	Arg	Thr	Val	Met	Pro	Gly	Phe	Asn	
145				150						155				160		
Tyr	Glu	Ala	Pro	Pro	Thr	Gln	His	Lys	Ile	Asn	Pro	Tyr	Asp	Ile	Thr	
			165					170						175		
Gly	Ala	Glu	Val	Leu	Lys	Tyr	Ile	Asp	Phe	Asn	Ala	Gly	Asn	Ile	Ala	
		180					185					190				
Lys	Gln	Leu	Leu	Asn	Gln	Phe	Glu	Gly	Phe	Ser	Pro	Leu	Ile	Thr	Asn	
	195						200					205				
Glu	Ile	Val	Ser	Arg	Arg	Gln	Phe	Met	Thr	Ser	Ser	Thr	Leu	Pro	Glu	
	210					215					220					
Ala	Phe	Asp	Glu	Val	Met	Ala	Glu	Thr	Lys	Leu	Pro	Pro	Thr	Pro	Ile	
225				230						235					240	
Phe	His	Lys	Asn	His	Glu	Thr	Gly	Lys	Glu	Asp	Phe	Tyr	Phe	Ile	Lys	
			245						250					255		
Leu	Asn	Gln	Phe	Asn	Asp	Asp	Thr	Val	Thr	Tyr	Asp	Ser	Leu	Asn	Asp	
		260					265						270			
Leu	Leu	Asp	Arg	Phe	Tyr	Asp	Ala	Arg	Gly	Glu	Arg	Glu	Arg	Val	Lys	
	275						280					285				

Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys
 290 295 300

Tyr Gln Asn Lys Leu Ala Ser
 305 310

(2) INFORMATION FOR SEQ ID NO:5222:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 245 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

Ile Ser Glu Leu Ile Glu Glu Tyr Glu Gln Ser Lys Asn Lys Asp Thr
 1 5 10 15
 Glu Gln Leu Tyr Gly Glu Leu Ile Thr Ala Asn Ile Tyr Arg Ile Lys
 20 25 30
 Gln Gly Asp Lys Glu Val Thr Ala Leu Asn Tyr Tyr Thr Asn Glu Glu
 35 40 45
 Val Val Ile Pro Leu Asn Pro Thr Lys Ser Pro Ser Ala Asn Ala Gln
 50 55 60
 Tyr Tyr Tyr Lys Gln Tyr Xaa Arg Met Lys Thr Arg Xaa Arg Glu Leu
 65 70 75 80
 Gln His Gln Ile Gln Leu Thr Lys Asp Asn Ile Asp Tyr Phe Ser Thr
 85 90 95
 Ile Glu Gln Gln Leu His His Ile Ser Val His Asp Ile Asp Glu Id
 100 105 110
 Arg Asp Glu Leu Ala Glu Gln Gly Phe Met Lys Gln Arg Lys Asn Gln
 115 120 125
 Thr Lys Lys Lys Lys Ala Gln Ile GlnLeu Gln His Tyr Val Ser Thr
 130 135 140
 Asp Gly Asp Asp Ile Tyr Val Gly Lys Asn Asn Lys Gln Asn Asp Tyr
 145 150 155 160
 Leu Thr Asn Lys Lys Ala Lys Lys Thr His Thr Trp Leu His Thr Lys
 165 170 175
 Asp Ile Pro Gly Ser His Val Val Ile Phe Asn Asp Ala Pro Ser Asp
 180 185 190
 Thr Thr Ile Lys Glu Ala Ala Met Leu Ala Gly Tyr Phe Ser Lys Ala
 195 200 205

Gly Asn Ser Gly Gln Ile Pro Val Asp Tyr Thr Leu Ile Lys Asn Val
 210 215 220

His Lys Pro Ser Gly Ala Lys Pro Gly Phe Val Thr Tyr Asp Asn Gln
 225 230 235 240

Lys Thr Leu Tyr Ala
 245

(2) INFORMATION FOR SEQ ID NO:5223:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ IDNO:5223:

Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser
 1 5 10 15

Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg
 20 25 30

Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu
 35 40 45

Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn
 50 55 60

Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe
 65 70 75 80

Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe Tyr Ile Lys Lys Tyr
 85 90 95

Asp Leu Lys

(2) INFORMATION FOR SEQ ID NO:5224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu

1	5	10	15
Ala Ile Gln His Arg Gly Glu Thr Val Thr Glu Gly Ser Ser Ser Asn	20	25	30
Ala Tyr Ala Ile Lys Asp Gly Val Ile Tyr Thr His Pro Ile Asn Asn	35	40	45
Tyr Ile Leu Asn Gly Ile Thr Arg Ile Val Ile Lys Lys Ile Ala Glu	50	55	60
Asp Tyr Asn Ile Pro Phe Lys Glu Glu Thr Phe Thr Val Asp Phe Leu	65	70	75
Lys Asn Ala Asp Glu Val Ile Val Ser Ser Thr Ser Ala Glu Val Thr	85	90	95
Pro Val Ile Lys Leu Asp Gly Glu Pro Val Asn Asp Gly Lys Val Gly	100	105	110
Pro Ile Thr Arg Gln Leu Gln Glu Gly Phe Glu Lys Tyr Ile Glu Ser	115	120	125
His Ser Ile	130		

(2) INFORMATION FOR SEQ ID NO:5225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn	5	10	15
Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile	20	25	30
Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr	35	40	45
Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala	50	55	60
Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln	65	70	75
Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro	85	90	95
Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly	100	105	110

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
 115 120 125
 Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
 130 135 140
 Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
 145 150 155 160
 Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
 165 170 175
 Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
 180 185 190
 Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
 195 200 205
 Pro Ala Ile Ser Thr Asp Glu Asn Arg Gln Asp Pro Thr Val Thr Val
 210 215 220
 Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly
 225 230 235 240
 Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn
 245 250 255
 Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val
 260 265 270
 Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys
 275 280 285
 Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr
 290 295 300
 Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp
 305 310 315 320
 Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly
 325 330 335
 Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu
 340 345 350
 Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr
 355 360 365
 Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly
 370 375 380
 Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro
 385 390 395 400
 Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn
 405 410 415
 Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu
 420 425 430

Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr
435 440 445

Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met His
450 455 460

Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly
465 470 475 480

Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp
485 490 495

Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr
500 505 510

Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser
515 520 525

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His
530 535 540

(2) INFORMATION FOR SEQ ID NO:5226:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His
1 5 10 15

Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val
20 25 30

Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile
35 40 45

Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His
50 55 60

Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe
65 70 75 80

Phe Phe Ile Ile Thr Ile Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe
85 90 95

Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu
100 105 110

Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly
115 120 125

Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro

130		135		140
Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile				
145		150		155 160
Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val				
	165		170	175
Lys				

(2) INFORMATION FOR SEQ ID NO:5227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile Gly Glu Phe Asn Ala			
1	5	10	15
Thr Gly Thr Lys Leu Leu Tyr Asn Lys Pro Ile Gln Gln Gln Leu Gln			
	20	25	30
His Ile Thr Tyr Ile Pro Gln Lys Ala His Ile Asp Leu Asp Phe Pro			
	35	40	45
Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys Tyr Lys Glu Ile Gly			
	50	55	60
Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp Lys Leu Lys Gln Leu			
	65	70	80
Leu Ser Asp Leu Glu Leu Glu Ser Leu Arg His Arg Gln Ile Ser Glu			
	85	90	95
Leu Ser Gly Gly Gln Leu Gln Arg Val Leu Val Ala Arg Ala Leu Met			
	100	105	110
Ser Xaa Ser Glu Val Tyr Phe Leu Asp Glu Pro Phe Val Gly Ile Asp			
	115	120	125
Phe Ser Ser Glu Lys Leu Ile Met Thr Lys Ile Glu Asn Leu LysGln			
	130	135	140
Gln Gly Lys Leu Ile Leu Ile Ile His His Asp Leu Ser Lys Ala Lys			
	145	150	155 160
Gln Tyr Phe Asp Arg Ile Ile Leu Leu Asn Gln Thr Leu Arg Tyr Phe			
	165	170	175
Gly Asp Ser Glu Glu Ala Met Ser Val Thr Arg Leu Asn Glu Thr Phe			
	180	185	190

Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr
 195 200 205

Cys

(2) INFORMATION FOR SEQ ID NO:5228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

Thr	Phe	Arg	Ile	Ile	Phe	Leu	Leu	Ser	Ile	Arg	Lys	Arg	Ser	Asn	Arg	1	5	10	15
Thr	His	Val	Ser	Ile	His	Trp	Ser	Thr	Val	Asn	Lys	Glu	Glu	Ile	Cys	20	25	30	
Leu	Arg	Val	Lys	Asp	Asn	Leu	Gln	Gln	Ile	Ser	Thr	Gln	Ile	Asn	Asp	35	40	45	
Lys	Ser	Glu	Lys	Asn	Asn	Phe	Ser	Thr	Lys	Pro	Asn	Val	Ile	Ala	Val	50	55	60	
Thr	Lys	Tyr	Val	Thr	Ile	Glu	Arg	Ala	Lys	Glu	Ala	Tyr	Glu	Ala	Gly	65	70	75	80
Ile	Arg	His	Phe	Gly	Glu	Asn	Arg	Leu	Glu	Gly	Phe	Phe	Gln	Lys	Lys	85	90	95	
Glu	Ala	Leu	Pro	Ser	Asp	Ala	Val	Ile	His	Phe	Ile	Gly	Ser	Leu	Gln	100	105	110	
Ser	Arg	Lys	Val	Lys	Asp	Val	Ile	Asn	Asp	Val	Asp	Tyr	Phe	His	Ala	115	120	125	
Leu	Asp	Arg	Leu	Ser	Leu	Ala	Lys	Glu	Ile	Asn	Lys	Arg	Ala	Glu	His	130	135	140	
Lys	Ile	Lys	Cys	Phe	Leu	Gln	Val	Asn	Val	Ser	Gly	Glu	Ala	Ser	Lys	145	150	155	160
His	Gly	Ile	Ala	Leu	Glu	Asp	Val	Asp	Gln	Phe	Ile	Asp	Asp	Leu	Lys	165	170	175	
Lys	Tyr	Asp	Lys	Ile	Glu	Ile	Val	Gly	Leu	Met	Thr	Met	Ala	Pro	Leu	180	185	190	
Thr	Asp	Asp	Glu	Ala	Tyr	Ile	Arg	Ser	Leu	Phe	Lys	Gln	Leu	Arg	Leu	195	200	205	

Lys Lys Glu Glu Ile Gln Arg Leu Asn Leu Glu Tyr Ala Pro Cys Asp
 210 215 220
 Glu Leu Ser Met Gly Met Ser Asn Asp Tyr Leu Ile Ala Val Glu Glu
 225 230 235 240
 Gly Ala Thr Phe Val Arg Ile Gly Thr Lys Leu Val Gly Glu Glu Glu
 245 250 255

(2) INFORMATION FOR SEQ ID NO:5229:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

Lys His Lys Leu Thr Ile Ile Thr Gly Gly Phe Phe Thr Met Lys Lys
 1 5 10 15
 Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val Thr Gly Tyr
 20 25 30
 Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val Asn Val Asp
 35 40 45
 Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp Gln Leu Asn
 50 55 60
 Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe Val Lys Asp
 65 70 75 80
 Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp Ser Trp Ser
 85 90 95
 Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn Val Ala Gly
 100 105 110
 Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val Gln Ser Val
 115 120 125
 Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala Val Ser Ala
 130 135 140
 Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg
 145 150 155 160
 Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln
 165 170 175
 Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile
 180 185 190

Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly
195 200 205

Ala Ser Gly Leu Phe Gln Thr Met ProGly Trp Gly Pro Thr Asn Thr
210 215 220

Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys Ala Gln Gly
225 230 235 240

Leu Gly Ala Trp Gly Phe
245

(2) INFORMATION FOR SEQ ID NO:5230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

Lys Glu Pro His Lys Met Lys Lys Ile Tyr Lys Ser Leu Thr Val Ser
1 5 10 15

Ala Ile Val Ala Thr Val Ser Leu Ser Ala Leu Pro Gln Ser Leu Ala
20 25 30

Ile Thr His Glu Ser Gln Pro Thr Lys Gln Gln Arg Thr Val Leu Phe
35 40 45

Asp Arg Ser His Gly Gln Thr Ala Gly Ala Ala Asp Trp Val Ser Asp
50 55 60

Gly Ala Phe Ser Asp Tyr Ala Asp Ser Ile Gln Lys Gln Gly Tyr Asp
65 70 75 80

Val Lys Ala Ile Asp Gly His Ser Asn Ile Thr Glu Ala Ser Leu Lys
85 90 95

Ser Ser Lys Ile Phe Val Ile Pro Glu Ala Asn Ile Pro Phe Lys Glu
100 105 110

Ser Glu Gln Ala Ala Ile Val Lys Tyr Val Lys Gln Gly Gly Asn Val
115 120 125

Val Phe Ile Ser Asp His Tyr Asn Ala Asp Arg Asn Leu Asn Arg Ile
130 135 140

Asp Ser Ser Glu Ala Met Asn Gly Tyr Arg Arg Gly Ala Tyr Glu Asp
145 150 155 160

Met Ser Lys Gly Met Asn Ala Glu Glu Lys Ser Ser Thr Ala Met Gln
165 170 175

Gly Val Lys Ser Ser Asp Trp Leu Ser Thr Asn Phe Gly Val Arg Phe

180										185					190				
Arg	Tyr	Asn	Ala	Leu	Gly	Asp	Leu	Asn	Thr	Ser	Asn	Ile	Val	Ser	Ser				
		195					200					205							
Lys	Glu	Ser	Phe	Gly	Ile	Thr	Glu	Gly	Val	Lys	Ser	Val	Ser	Met	His				
	210					215					220								
Ala	Gly	Ser	Thr	Leu	Ala	Ile	Thr	Asn	Pro	Glu	Lys	Ala	Lys	Gly	Ile				
225					230					235					240				
Val	Tyr	Thr	Pro	Glu	Gln	Leu	Pro	Ala	Lys	Ser	Lys	Trp	Ser	His	Ala				
				245					250					255					
Val	Asp	Gln	Gly	Ile	Tyr	Asn	Gly	Gly	Gly	Lys	Ala	Glu	Gly	Pro	Tyr				
			260					265						270					
Val	Ala	Ile	Ser	Lys	Val	Gly	Lys	Gly	Lys	Ala	Ala	Phe	Ile	Gly	Asp				
	275						280					285							
Ser	Ser	Leu	Val	Glu	Asp	Ser	Ser	Pro	Lys	Tyr	Val	Arg	Glu	Asp	Asn				
	290					295					300								
Gly	Glu	Lys	Lys	Lys	Thr	Tyr	Asp	Gly	Phe	Lys	Glu	En	Asp	Asn	Gly				
305					310					315					320				
Lys	Leu	Leu	Asn	Asn	Ile	Thr	Ala	Trp	Met	Ser	Lys	Asp	Asn	Asp	Gly				
			325					330					335						
Lys	Ser	Leu	Lys	Ala	Ser	Ser	Leu	Thr	Leu	Asp	Thr	Lys	Thr	Lys	Leu				
			340					345					350						
Leu	Asp	Phe	Glu	Arg	Pro	Glu	Arg	Ser	Thr	Glu	Pro	Glu	Lys	Glu	Pro				
	355						360					365							
Trp	Ser	Gln	Pro	Pro	Ser	Gly	Tyr	Lys	Trp	Tyr	Asp	Pro	Thr	Thr	Phe				
	370					375					380								
Lys	Ala	Gly	Ser	Tyr	Gly	Ser	Glu	Lys	Gly	Ala	Asp	Pro	Gln	Pro	Asn				
385					390					39					400				
Thr	Pro	Asp	Asp	His	Thr	Pro	Pro	Asn	Gln	Asn	Glu	Lys	Val	Thr	Phe				
				405					410					415					
Asp	Ile	Pro	Gln	Asn	Val	Ser	Val	Asn	Glu	Pro	Phe	Glu	Met	Thr	Ile				
			420					425					430						
His	Leu	Lys	Gly	Phe	Glu	Ala	Asn	Gln	Thr	Leu	Glu	Asn	Leu	Arg	Val				
	435						440					445							
Gly	Ile	Tyr	Lys	Glu	Gly	Gly	Arg	Gln	Ile	Gly	Gln	Phe	Ser	Ser	Lys				
	450					455					460								
Asp	Asn	Asp	Tyr	Asn	Pro	Pro	Gly	Tyr	Ser	Thr	Leu	Pro	Thr	Val	Lys				
465					470					475					480				
Ala	Asp	Glu	Asn	Gly	Asn	Val	Thr	Ile	Lys	Val	Asn	Ala	Lys	Val	Leu				
				485					490					495					
Glu	Ser	Met	Glu	Gly	Ser	Lys	Ile	Arg	Leu	Lys	Leu	Gly	Asp	Lys	Thr				
			500					505					510						

Leu Ile Thr Thr Asp Phe Lys
515

(2) INFORMATION FOR SEQ ID NO:5231:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

Arg	Asp	Glu	Arg	Ile	Lys	Thr	Met	Thr	Asn	Ser	Ser	Lys	Ser	Phe	Thr	
1				5					10					15		
Lys	Phe	Met	Ala	Ala	Ser	Ala	Val	Phe	Thr	Met	Gly	Phe	Leu	Ser	Val	
			20					25					30			
Pro	Thr	Ala	Gly	Ala	Glu	Gln	Thr	Asn	Gln	Ile	Ala	Asn	Lys	Pro	Gln	
		35					40					45				
Ala	Ile	Gln	Trp	His	Thr	Asn	Leu	Thr	Asn	Glu	Arg	Phe	Thr	Thr	Ile	
	50					55					60					
Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Ala	Pro	Glu	His	Thr	Phe	Gln	Ala	
65					70				75					80		
Tyr	Asp	Lys	Ser	His	Asn	Glu	Leu	Lys	Ala	Ser	Tyr	Ile	Glu	Ile	Asp	
				85					90					95		
Leu	Gln	Arg	Thr	Lys	Asp	Gly	His	Leu	Val	Ala	Met	His	Asp	Glu	Thr	
			100					105					110			
Val	Asn	Arg	Thr	Thr	Asn	Gly	His	Gly	Lys	Val	Glu	Asp	Tyr	Thr	Leu	
		115					120					125				
Asp	Glu	Leu	Lys	Gln	Leu	Asp	Ala	Gly	Ser	Trp	Phe	Asn	Lys	Lys	Tyr	
	130					135					140					
Pro	Lys	Tyr	Ala	Arg	Ala	Ser	Tyr	Lys	Asn	Ala	Lys	Val	Pro	Thr	Leu	
145					150					155					160	
Asp	Glu	Ile	Leu	Glu	Arg	Tyr	Gly	Pro	Asn	Ala	Asn	Tyr	Tyr	Ile	Glu	
			165						170					175		
Thr	Lys	Ser	Pro	Asp	Val	Tyr	Pro	Gly	Met	Glu	Glu	Gln	Leu	Leu	Ala	
			180					185					190			
Ser	Leu	Lys	Lys	His	His	Leu	Leu	Asn	Asn	Asn	Lys	Leu	Lys	Asn	Gly	
		195					200					205				
His	Val	Met	Ile	Gln	Ser	Phe	Ser	Asp	Glu	Ser	Leu	Lys	Lys	Ile	His	
	210					215					220					

Arg Gln Asn Lys His Val Pro Leu Val Lys Leu Val Asp Lys Gly Glu
 225 230 235 240
 Leu Gln Gln Phe Asn Asp Gln Arg Leu Lys Glu Ile Arg Ser Tyr Ala
 245 250 255
 Ile Gly Leu Gly Pro Asp Tyr Thr Asp Leu Thr Glu Gln Asn Thr His
 260 265 270
 His Leu Lys Asp Leu Gly Phe Ile Val His Pro Tyr Thr Val Asn Glu
 275 280 285
 Lys Ala Asp Met Leu Arg Leu Asn Lys Tyr Gly Val Asp Gly Val Phe
 290 295 300
 Thr Asn Phe Ala Asp Lys Tyr Lys Glu Val Ile Lys
 305 310 315

(2) INFORMATION FOR SEQ ID NO:5232:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 433 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

Arg Phe Met Lys Asn Leu Ile Ser Ile Ile Ile Ile Leu Cys Leu Thr
 1 5 10 15
 Leu Ser Ile Met Thr Pro Tyr Ala Gln Ala Thr Asn Ser Asp Val Thr
 20 25 30
 Pro Val Gln Ala Ala Asn Gln Tyr Gly Tyr Ala Gly Leu Ser Ala Ala
 35 40 45
 Tyr Glu Pro Thr Ser Ala Val Asn Val Ser Gln Thr Gly Gln Leu Leu
 50 55 60
 Tyr Gln Tyr Asn Ile Asp Thr Lys Trp Asn Pro Ala Ser Met Thr Lys
 65 70 75 80
 Leu Met Thr Met Tyr Leu Thr Leu Glu Ala Val Asn Lys Gly Gln Leu
 85 90 95
 Ser Leu Asp Asp Thr Val Thr Met Thr Asn Lys Glu Tyr Ile Met Ser
 100 105 110
 Thr Leu Pro Glu Leu Ser Asn Thr Lys Leu Tyr Pro Gly Gln Val Trp
 115 120 125
 Thr Ile Ala Asp Leu Leu Gln Ile Thr Val Ser Asn Ser Ser Asn Ala
 130 135 140
 Ala Ala Leu Ile Leu Ala Lys Lys Val Ser Lys Asn Thr Ser Asp Phe

145		150		155		160									
Val	Asp	Leu	Met	Asn	Asn	Lys	Ala	Lys	Ala	Ile	Gly	Met	Lys	Asn	Thr
				165					170					175	
His	Phe	Val	Asn	Pro	Thr	Gly	Ala	Glu	Asn	Ser	Arg	Leu	Arg	Thr	Phe
			180					185					190		
Ala	Pro	Thr	Lys	Tyr	Lys	Asp	Gln	Glu	Arg	Thr	Val	Thr	Thr	Ala	Arg
		195					200					205			
Asp	Tyr	Ala	Ile	Leu	Asp	Leu	His	Val	Ile	Lys	Glu	Thr	Pro	Lys	Ile
	210					215					220				
Leu	Asp	Phe	Thr	Lys	Gln	Leu	Ala	Pro	Thr	Thr	His	Ala	Val	Thr	Tyr
225					230					235					240
Tyr	Thr	Phe	Asn	Phe	Ser	Leu	Glu	Gly	Ala	Lys	Met	Ser	Leu	Pro	Gly
			245						250					255	
Thr	Asp	Gly	Leu	Lys	Thr	Gly	Ser	Ser	Asp	Thr	Ala	Asn	Tyr	Asn	His
			260					265					270		
Thr	Ile	Thr	Thr	Lys	Arg	Gly	Lys	Phe	Arg	Ile	Asn	Gln	Val	Ile	Met
	275						280					285			
Gly	Ala	Gly	Asp	Tyr	Lys	Asn	Leu	Gly	Gly	Glu	Lys	Gln	Arg	Asn	Met
	290					295					300				
Met	Gly	Asn	Ala	Leu	Met	Glu	Arg	Ser	Phe	Asp	Gln	Tyr	Lys	Tyr	Val
305					310					315					320
Lys	Ile	Leu	Ser	Lys	Gly	Glu	Gln	Arg	Ile	Asn	Gly	Lys	Lys	Tyr	Tyr
				325					330					335	
Val	Glu	Asn	Asp	Leu	Tyr	Asp	Val	Leu	Pro	Ser	Asp	Phe	Ser	Lys	Lys
			340					345					350		
Asp	Tyr	Lys	Leu	Val	Val	Glu	Asp	Gly	Lys	Val	His	Ala	Asp	Tyr	Pro
		355					360					365			
Arg	Glu	Phe	Ile	Asn	Lys	Asp	Tyr	Gly	Pro	Pro	Thr	Val	Glu	Val	His
	370					375					380				
Gln	Pro	Ile	Ile	Gln	Lys	Ala	Asn	Thr	Val	Ala	Lys	Ser	Met	Trp	Glu
385					390					395					400
Glu	His	Pro	Leu	Phe	Thr	Ile	Ile	Gly	Gly	Thr	Cys	Leu	Val	Ala	Gly
				405					410					415	
Leu	Ala	Leu	Ile	Val	His	Met	Ile	Ile	Asn	Arg	Leu	Phe	Arg	Lys	Arg
			420					425					430		

Lys

(2) INFORMATION FOR SEQ ID NO:5233:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

Leu Thr Lys Glu Arg Glu Tyr Met Lys Leu Lys Ser Phe Ile Thr Val
1 5 10 15
Thr Leu Ala Leu Gly Met Ile Ala Thr Thr Gly Ala Thr Val Ala Gly
20 25 30
Asn Glu Val Ser Ala Ala Glu Lys Asp Lys Leu Pro Ala Thr Gln Lys
35 40 45
Ala Lys Glu Met Gln Asn Val Pro Tyr Thr Ile Ala Val Asp Gly Ile
50 55 60
Met Ala Phe Asn Gln Ser Tyr Leu Asn Leu Pro Lys Asp Ser Gln Leu
65 70 75 80
Ser Tyr Leu Asp Leu Gly Asn Lys Val Lys Ala Leu Leu Tyr Asp Glu
85 90 95
Arg Gly Val Thr Pro Glu Lys Ile Arg Asn Ala Lys Ser Ala Val Tyr
100 105 110
Thr Ile Thr Trp Lys Asp Gly Ser Lys Lys Glu Val Asp Leu Lys Lys
115 120 125
Asp Ser Tyr Thr Ala Asn Leu Phe Asp Ser Asn Ser Ile Lys Gln Ile
130 135 140
Asp Ile Asn Val Lys Thr Lys
145 150

(2) INFORMATION FOR SEQ ID NO:5234:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 497 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

Asn His Cys Asn Arg Ile Glu Arg Lys Met Ala Met Ser Asn Asn Phe
1 5 10 15
Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile Asp Thr Asn Ser His
20 25 30

Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln Ser Glu Leu Glu His
 35 40 45
 Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe Pro Pro Arg Asn Ala
 50 55 60
 Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr Asn His Asn Lys Gln
 65 70 75 80
 Val His Asn Glu Ser Gln Thr Ser Glu Asp Asn Val Gln Asn Glu Ala
 85 90 95
 Gly Thr Ile Asp Asp Arg Gln Val Glu Ser Ser His Ser Thr Glu Ser
 100 105 110
 Gln Glu Pro Ser His Gln Asp Ser Thr Pro Gln His Glu Glu Glu Tyr
 115 120 125
 Tyr Asn Lys Asn Ala Phe Ala Met Asp Lys Ser His Pro Glu Pro Ile
 130 135 140
 Glu Asp Asn Asp Lys His Asp Thr Ile Lys Asn Ala Glu Asn Asn Thr
 145 150 155 160
 Glu His Ser Thr Val Ser Asp Lys Ser Glu Ala Glu Gln Ser Gln Gln
 165 170 175
 Pro Lys Pro Tyr Phe Thr Thr Gly Ala Asn Gln Ser Glu Thr Ser Lys
 180 185 190
 Asn Glu His Asp Asn Asp Ser Val Lys Gln Asp Gln Asp Glu Pro Lys
 195 200 205
 Glu His His Asn Gly Lys Lys Ala Ala Ala Ile Gly Ala Gly Thr Ala
 210 215 220
 Gly Val Ala Gly Ala Ala Gly Ala Met Ala Ala Ser Lys Ala Lys Lys
 225 230 235 240
 His Ser Asn Asp Ala Gln Asn Lys Ser Asn Ser Gly Lys Ala Asn Asn
 245 250 255
 Ser Thr Glu Asp Lys Ala Ser Gln Asp Lys Ser Lys Asp His His Asn
 260 265 270
 Gly Lys Lys Gly Ala Ala Ile Gly Ala Gly Thr Ala Gly Leu Ala Gly
 275 280 285
 Gly Ala Ala Ser Lys Ser Ala Ser Ala Ala Ser Lys Pro His Ala Ser
 290 295 300
 Asn Asn Ala Ser Gln Asn His Asp Glu His Asp Asn His Asp Arg Asp
 305 310 315 320
 Lys Glu Arg Lys Lys Gly Gly Met Ala Lys Val Leu Leu Pro Leu Ile
 325 330 335
 Ala Ala Val Leu Ile Ile Gly Ala Leu Ala Ile Phe Gly Gly Met Ala
 340 345 350
 Leu Asn Asn His Asn Asn Gly Thr Lys Glu Asn Lys Ile Ala Asn Thr

355		360		365
Asn Lys Asn Asn Ala Asp Glu Ser Lys Asp Lys Asp Thr Ser Lys Asp				
370		375		380
Ala Ser Lys Asp Lys Ser Lys Ser Thr Asp Ser Asp Lys Ser Lys Glu				
385		390		395 400
Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn				
	405		410	415
Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln Gln				
	420		425	430
Ala Asn Gln Asn Gln Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln				
	435		440	445
Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln				
	450		455	460
Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala				
465		470		475 480
Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile				
	485		490	495
Pro				

(2) INFORMATION FOR SEQ ID NO:5235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu Leu Ser Ile Lys Tyr Asn Leu Ile Gly Val Val Asn Asn Met Asn				
1	5		10	15
Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr				
	20		25	30
Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser				
	35		40	45
Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Th Ser Asp Lys Ile				
	50		55	60
Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp				
65		70		75 80
Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn				
	85		90	95

Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala
100 105 110
Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe
115 120 125
Gln Leu Leu Asp Lys Asn Asn Glu Thr Gln Tyr Tyr His Phe Phe Ser
130 135 140
Ile Lys Asp Pro Ala Asp Val Tyr Tyr Thr Lys Lys Lys Ala Glu Val
145 150 155 160
Glu Leu Asp Ile Asn Thr Ala Ser Thr Trp Lys Lys Phe Glu Val Tyr
165 170 175
Glu Asn Asn Gln Lys Leu Pro Val Arg Leu Val Ser Tyr Ser Pro Val
180 185 190
Pro Glu Asp His Ala Tyr Ile Arg Phe Pro Val Ser Asp Gly Trp Gln
195 200 205
Glu Leu Lys Ile Val Ser Ser Thr Gln Ile Asp Asp Gly Glu Glu Thr
210 215 220
Asn Tyr Asp Tyr Thr Lys Leu Val Phe Ala Lys Pro Ile Tyr Asn Asp
225 230 235 240
Pro Ser Leu Val Lys Ser Asp Thr Asn Asp Ala Val Val Thr Asn Asp
245 250 255
Gln Ser Ser Ser Val Ala Ser Asn Gln Thr Asn Thr Asn Thr Ser Asn
260 265 270
Gln Asn Ile Ser Thr Ile Asn Asn Ala Asn Asn Gln Pro Gln Ala Thr
275 280 28
Thr Asn Met Ser Gln Pro Ala Gln Pro Lys Ser Ser Thr Asn Ala Asp
290 295 300
Gln Ala Ser Ser Gln Pro Ala His Glu Thr Asn Ser Asn Gly Asn Thr
305 310 315 320
Asn Asp Lys Thr Asn Glu Ser Ser Asn Gln Ser Asp Val Asn Gln Gln
325 330 335
Tyr Pro Pro Ala Asp Glu Ser Leu Gln Asp Ala Ile Lys Asn Pro Ala
340 345 350
Ile Ile Asp Lys Glu His Thr Ala Asp Asn Trp Arg Pro Ile Asp Phe
355 360 365
Gln Met Lys Asn Asp Lys Gly Glu Arg Gln Ph Tyr His Tyr Ala Ser
370 375 380
Thr Val Glu Pro Ala Thr Val Ile Phe Thr Lys Thr Gly Pro Ile Ile
385 390 395 400
Glu Leu Gly Leu Lys Thr Ala Ser Thr Trp Lys Lys Phe Glu Val Tyr
405 410 415

Glu Gly Asp Lys Lys Leu Pro Val Glu Leu Val Ser Tyr Asp Ser Asp
 420 425 430
 Lys Asp Tyr Ala Tyr Ile Arg Phe Pro Val Ser Asn Gly Thr Arg Glu
 435 440 445
 Val Lys Ile Val Ser Ser Ile Glu Tyr Gly Glu Asn Ile His Glu Asp
 450 455 460
 Tyr Asp Tyr Thr Leu Met Val Phe Ala Gln Pro Ile Thr Asn Asn Pro
 465 470 475 480
 Asp Asp Tyr Val Asp Glu Glu Thr Tyr Asn Leu Gln Lys Leu Leu Ala
 485 490 495
 Pro Tyr His Lys Ala Lys Thr Leu Glu Arg Gln Val Tyr Glu Leu Glu
 500 505 510
 Lys Leu Gln Glu Lys Leu Pro Glu Lys Tyr Lys Ala Glu Tyr Lys Lys
 515 520 525
 Lys Leu Asp Gln Thr Arg Val Glu Leu Ala Asp Gln Val Lys Ser Ala
 530 535 540
 Val Thr Glu Phe Glu Asn Val Thr Pro Thr Asn Asp Gln Leu Thr Asp
 545 550 555 560
 Leu Gln Glu Ala His Phe Val Val Phe Glu Ser Glu Glu Asn Ser Glu
 565 570 575
 Ser Val Met Asp Gly Phe Val Glu His Pro Phe Tyr Thr Ala Thr Leu
 580 585 590
 Asn Gly Gln Lys Tyr Val Val Met Lys Thr Lys Asp Asp Ser Tyr Trp
 595 600 605
 Lys Asp Leu Ile Val Glu Gly Lys Arg Val Thr Thr Val Ser Lys Asp
 610 615 620
 Pro Lys Asn Asn Ser Arg Thr Leu Ile Phe Pro Tyr Ile Pro Asp Lys
 625 630 635 640
 Ala Val Tyr Asn Ala Ile Val Lys Val Val Val Ala Asn Ile Gly Tyr
 645 650 655
 Glu Gly Gln Tyr His Val Arg Ile Ile Asn Gln Asp Ile Asn Thr Lys
 660 665 670
 Asp Asp Asp Thr Ser Gln Asn Asn Thr Ser Glu Pro Leu Asn Val Gln
 675 680 685
 Thr Gly Gln Glu Gly Lys Val Ala Asp Thr Asp Val Ala Glu Asn Ser
 690 695 700
 Ser Thr Ala Thr Asn Pro Lys Asp Ala Ser Asp Lys Ala Asp Val Ile
 705 710 715 720
 Glu Pro Glu Ser Asp Val Val Lys Asp Ala Asp Asn Asn Ile Asp Lys
 725 730 735
 Asp Val Gln His Asp Val Asp His Leu Ser Asp Met Ser Asp Asn Asn

Gly Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys
 100 105 110
 Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu
 115 120 125
 Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys
 130 135 140
 Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys GlyAla Gln Thr
 145 150 155 160
 Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly
 165 170 175
 Thr Phe Met Glu Phe Asp Ah Tyr Ala Gln Pro Gly Asn Ser Gly Ser
 180 185 190
 Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly
 195 200 205
 Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro
 210 215 220
 Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys
 225 230 235

(2) INFORMATION FOR SEQ ID NO:5237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr
 1 5 10 15
 Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr
 20 25 30
 Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val
 35 40 45
 Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr AlaGly
 50 55 60
 Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr
 65 70 75 80
 Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala
 85 90 95

Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr
 100 105 110
 Leu Asn Ile Ser Ala Thr Pro Ala Pro Lys Gln Glu Gln Ser Gln Thr
 115 120 125
 Thr Thr Glu Ser Thr Thr Pro Lys Thr Lys Val Thr Thr Pro Pro Ser
 130 135 140
 Thr Asn Thr Pro Gln Pro Met Gln Ser Thr Lys Ser Asp Thr Pro Gln
 145 150 155 160
 Ser Pro Thr Ile Lys Gln Ala Gln Thr Asp Met Thr Pro Lys Tyr Glu
 165 170 175
 Asp Leu Arg Ala Tyr Tyr Thr Lys Pro Ser Phe Glu Phe Glu Lys Gln
 180 185 190
 Phe Gly Phe Met Leu Lys Pro Trp Thr Thr Val Arg Phe Met Asn Val
 195 200 205
 Ile Pro Asn Arg Phe Ile Tyr Lys Ile Ala Leu Val Gly Lys Asp Glu
 210 215 220
 Lys Lys Tyr Lys Asp Gly Pro Tyr Asp Asn Ile Asp Val Phe Ile Val
 225 230 235 240
 Leu Glu Asp Asn Lys Tyr Gln Leu Lys Lys Tyr Ser Val Gly Gly Ile
 245 250 255
 Thr Lys Thr Asn Ser Lys Lys Val Asn His Lys Val Glu Leu Ser Ile
 260 265 270
 Thr Lys Lys Asp Asn Gln Gly Met Ile Ser Arg Asp Val Ser Glu Tyr
 275 280 285
 Met Ile Thr Lys Glu Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Leu
 290 295 300
 Arg Lys Gln Leu Ile Glu Lys His Asn Leu Tyr Gly Asn Met Gly Ser
 305 310 315 320
 Gly Thr Ile Val Ile Lys Met Lys Asn Gly Gly Lys Tyr Thr Phe Glu
 325 330 335
 Leu His Lys Lys Leu Gln Glu His Arg Met Ala Asp Val Ile Asp Gly
 340 345 350
 Thr Asn Ile Asp Asn Ile Glu Val Asn Ile Lys
 355 360

(2) INFORMATION FOR SEQ ID NO:5238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu GlyVal
1 5 10 15
Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala
20 25 30
Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser
35 40 45
Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn
50 55 60
Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys
65 70 75 80
Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile
85 90 95
Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr
100 105 110
Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr
115 120 125
Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn
130 135 140
Val Asp Thr Lys Lys Gln
145 150

(2) INFORMATION FOR SEQ ID NO:5239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp
1 5 10 15
Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Glu Gly
20 25 30
Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile
35 40 45
Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gl
50 55 60

Arg Asp Gly Met Glu Val Cys Arg Glu Val Arg Lys Lys Tyr Glu Met
 65 70 75 80
 Pro Ile Ile Met Leu Thr Ala Lys Asp Ser Glu Ile Asp Lys Val Leu
 85 90 95
 Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser Thr
 100 105 110
 Arg Glu Leu Ile Ala Arg Val Lys Ala Asn Leu Arg Arg His Tyr Ser
 115 120 125
 Gln Pro Ala Gln Asp Thr Gly Asn Val Thr Asn Glu Ile Thr Ile Lys
 130 135 140
 Asp Ile Val Ile Tyr Pro Asp Ala Tyr Ser Ile Lys Lys Arg Gly Glu
 145 150 155 160
 Asp Ile Glu Leu Thr His Arg Glu Phe Glu Leu Phe His Tyr Leu Ser
 165 170 175
 Lys His Met Gly Gln Val Met Thr Arg Glu His Leu Leu Gln Thr Val
 180 185 190
 Trp Gly Tyr Asp Tyr Phe Gly Asp Val Arg Thr Val Asp Val Thr Ile
 195 200 205
 Arg Arg Leu Arg Glu Lys Ile Glu Asp Asp Pro Ser His Pro Glu Tyr
 210 215 220
 Ile Val Thr Arg Arg Gly Val Gly Tyr Phe Leu Gln Gln His Glu
 225 230 235

(2) INFORMATION FOR SEQ ID NO:5240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:

Xaa Leu Ser Thr Val Ile Gly Ala Xaa Leu Phe Phe Lys Ser Ser Val
 1 5 10 15
 Ser Leu Val Phe Lys Met Val Lys Lys Phe Arg Xaa Gly Val Ile Ser
 20 25 30
 Val Asn Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys
 35 40 45
 Asn Ala Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val
 50 55 60

Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu
 65 70 75 80
 Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys
 85 90 95
 Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile ProHis Phe
 100 105 110
 Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu
 115 120 125
 Phe Asp Val Lys Ala
 130

(2) INFORMATION FOR SEQ ID NO:5241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 508 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val
 1 5 10 15
 Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe IleAsn Gly
 20 25 30
 Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro
 35 40 45
 Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp
 50 55 60
 Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser
 65 70 75 80
 Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp
 85 90 95
 Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn
 100 105 110
 Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala
 115 120 125
 Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly
 130 135 140
 Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu
 145 150 155 160
 Pro Ile Gly Val Val Gly Ala Val Val Ala Trp Asn Phe Pro Met Leu

165										170					175				
Leu	Ala	Ala	Trp	Lys	Ile	Ala	Pro	Ala	Ile	Ala	Ala	Gly	Asn	Thr	Ile				
			180					185					190						
Val	Ile	Gln	Pro	Ser	Ser	Ser	Thr	Pro	Leu	Ser	Leu	Leu	Glu	Val	Ala				
		195					200					205							
Lys	Ile	Phe	Gln	Glu	Val	Leu	Pro	Lys	Gly	Val	Val	Asn	Ile	Leu	Thr				
	210					215					220								
Gly	Lys	Gly	Ser	Glu	Ser	Gly	Asn	Ala	Ile	Phe	Asn	His	Asp	Gly	Val				
225					230					235					240				
Asp	Lys	Leu	Ser	Phe	Thr	Gly	Ser	Thr	Asp	Val	Gly	Tyr	Gln	Val	Ala				
				245					250					255					
Glu	Ala	Ala	Ala	Lys	His	Leu	Val	Pro	Ala	Thr	Leu	Glu	Leu	Gly	Gly				
			260					265					270						
Lys	Ser	Ala	Asn	Ile	Ile	Leu	Asp	Asp	Ala	Asn	Leu	Asp	Leu	Ala	Val				
		275					280					285							
Glu	Gly	Ile	Gln	Leu	Gly	Ile	Leu	Phe	Asn	Gln	Gly	Glu	Val	Cys	Ser				
	290					295					300								
Ala	Gly	Ser	Arg	Leu	Leu	Val	His	Glu	Lys	Ile	Tyr	Asp	Gln	Leu	Val				
305					310					315					320				
Pro	Arg	Leu	Gln	Glu	Ala	Phe	Ser	Asn	Ile	Lys	Val	Gly	Asn	Pro	Gln				
				325					330					335					
Asp	Glu	Ala	Thr	Gln	Met	Gly	Ser	Gln	Thr	Gly	Lys	Asp	Gln	Leu	Asp				
			340					345					350						
Lys	Ile	Gln	Ser	Tyr	Ile	Asp	Ala	Ala	Lys	Glu	Ser	Asp	Ala	Gln	Ile				
		355				360						365							
Leu	Ala	Gly	Gly	His	Arg	Leu	Thr	Glu	Asn	Gly	Leu	Asp	Lys	Gly	Phe				
	370					375						380							
Phe	Phe	Glu	Pro	Thr	Leu	Ile	Ala	Val	Pro	Asp	Asn	His	His	Lys	Leu				
385					390					395					400				
Ala	Gln	Glu	Glu	Ile	Phe	Gly	Pro	Val	Leu	Thr	Val	Ile	Lys	Val	Lys				
				405					410					415					
Asp	Asp	Gln	Glu	Ala	Ile	Asp	Ile	Ala	Asn	Asp	Ser	Glu	Tyr	Gly	Leu				
			420					425					430						
Ala	Gly	Gly	Val	Phe	Ser	Gln	Asn	Ile	Thr	Arg	Ala	Leu	Asn	Ile	Ala				
		435					440					445							
Lys	Ala	Val	Arg	Thr	Gly	Arg	Ile	Trp	Ile	Asn	Thr	Tyr	Asn	Gln	Val				
	450					455					460								
Pro	Glu	Gly	Ala	Pro	Phe	Gly	Gly	Tyr	Lys	Lys	Ser	Gly	Ile	Gly	Arg				
465					470					475					480				
Glu	Thr	Tyr	Lys	Gly	Ala	Leu	Ser	Asn	Tyr	Gln	Gln	Val	Lys	Asn	Ile				
				485					490					495					

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr
500 505

(2) INFORMATION FOR SEQ ID NO:5242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn	His	Leu	Thr	Ala	Arg	Ile	Ile	Asn	Gln	Glu	Asp	Asp	Leu	Met	Asn	1	5	10	15
Leu	Phe	Arg	Gln	Gln	Lys	Phe	Ser	Ile	Arg	Lys	Phe	Asn	Val	Gly	Ile	20	25	30	
Phe	Ser	Ala	Leu	Ile	Ala	Thr	Val	Thr	Phe	Ile	Ser	Thr	Asn	Pro	Thr	35	40	45	
Thr	Ala	Ser	Ala	Ala	Glu	Gln	Asn	Gln	Pro	Ala	Gln	Asn	Gln	Pro	Ala	50	55	60	
Gln	Pro	Ala	Asp	Ala	Asn	Thr	Gln	Pro	Asn	Ala	Asn	Ala	Gly	Ala	Gln	65	70	75	80
Ala	Asn	Pro	Thr	Ala	Gln	Pro	Ala	Ala	Pro	Ala	Asn	Gln	Gly	Gln	Pro	85	90	95	
Ala	Val	Gln	Pro	Ala	Asn	Gln	Gly	Gly	Gln	Ala	Asn	Pro	Ala	Gly	Gly	100	105	110	
Ala	Ala	Gln	Pro	Asn	Thr	Gln	Pro	Ala	Gly	Gln	Gly	Asp	Gln	Ala	Asp	115	120	125	
Pro	Asn	Asn	Ala	Ala	Gln	Ala	Gln	Pro	Gly	Asn	Gln	Ala	Thr	Pro	Ala	130	135	140	
Asn	Gln	Ala	Gly	Gln	Gly	Asn	Asn	Gln	Ala	Thr	Pro	Asn	Asn	Asn	Ala	145	150	155	160
Thr	Pro	Ala	Asn	Gln	Thr	Gln	Pro	Ala	Asn	Ala	Pro	Ala	Ala	Ala	Gln	165	170	175	
Pro	Ala	Ala	Pro	Val	Ala	Ala	Asn	Ala	Gln	Thr	Gln	Asp	Pro	Asn	Ala	180	185	190	
Ser	Asn	Thr	Gly	Glu	Gly	Ser	Ile	Asn	Thr	Thr	Leu	Thr	Phe	Asp	Asp	195	200	205	
Pro	Ala	Ile	Ser	Thr	Asp	Glu	Asn	Arg	Gln	Asp	Pro	Thr	Val	Thr	Val	210	215	220	

Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly
 225 230 235 240
 Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn
 245 250 255
 Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val
 260 265 270
 Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys
 275 280 285
 Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr
 290 295 300
 Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp
 305 310 315 320
 Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly
 325 330 335
 Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu
 340 345 350
 Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr
 355 360 365
 Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly
 370 375 380
 Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro
 385 390 395 400
 Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn
 405 410 415
 Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu
 420 425 430
 Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr
 435 440 445
 Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr
 450 455 460
 Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly
 465 470 475 480
 Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp
 485 490 495
 Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr
 500 505 510
 Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser
 515 520 525
 Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His
 530 535 540

(2) INFORMATION FOR SEQ ID NO:5243:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 274 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

```

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln
1           5           10           15

Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln
          20           25           30

Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly
          35           40           45

Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp
50           55           60

Met Ile His His Gly Arg Ala Val Arg Arg Gly AlaPro Asn Thr Phe
65           70           75           80

Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln
          85           90           95

Asp Leu Asn His Ala Leu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala
          100          105          110

Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr
          115          120          125

Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser
          130          135          140

Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala
          145          150          155          160

Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val
          165          170          175

Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser
          180          185          190

Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr
          195          200          205

Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu
          210          215          220

His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe Ser Val Gly Val
          225          230          235          240

Asp Gly Leu Lys Gln Tyr Asp GlnGlu Val Lys Ser Gly Ala Phe Pro
          245          250          255

```

Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn
260 265 270

Asn Asp

(2) INFORMATION FOR SEQ ID NO:5244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val
1 5 10 15

Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn PheSer Ile
20 25 30

Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly
35 40 45

Met His Ile Gly Leu Arg Ala Asn Lys Lys Asp Phe Gly Trp Ile Tyr
50 55 60

Ser Ser Ser Leu Ala Ser Ala Ala Ala Val Tyr Thr Leu Asn Gln Phe
65 70 75 80

Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys
85 90 95

Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys
100 105 110

Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val
115 120 125

Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr
130 135 140

Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr
145 150 155 160

Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu
165 170 175

Ala Ile Leu Thr Thr Asp Thr Cys Thr Lys His Ile Ala Val Ser Leu
180 185 190

Lys Ile Asp Gly Lys Thr Val Thr Ile Gly Gy Ser Thr Lys Gly Ser
195 200 205

Gly Met Ile His Pro Asn Met Ala Thr Met Leu Ala Phe Ile Thr Thr
 210 215 220
 Asp Ala Ser Ile Glu Ser Asn Thr Leu His Gln Leu Leu Lys Ser Ser
 225 230 235 240
 Thr Asp His Thr Phe Asn Met Ile Thr Val Asp Gly Asp Thr Ser Thr
 245 250 255
 Asn Asp Met Val Leu Val Met Ala Asn His Gln Val Glu His Gln Ile
 260 265 270
 Leu Ser Gln Asp His Pro Gln Trp Glu Thr Phe Val Asp Ala Phe Asn
 275 280 285
 Phe Val Cys Thr Phe Leu Ala Lys Ala Ile Ala Arg Asp Gly Glu Gly
 290 295 300
 Ala Thr Lys Leu Ile Ser Val Asn Val Ser Gly Ala Lys Ser Ile Ser
 305 310 315 320
 Asp Ala Arg Lys Ile Gly Lys Thr Ile Val Ser Ser Asn Leu Val Lys
 325 330 335
 Ser Ala Ile Phe Gly Glu Asp Ala Asn Phe Gly Arg Ile Ile Thr Ala
 340 345 350
 Ile Gly Tyr Ser Gly Cys Glu Ile Asp Pro Asn Cys Thr Tyr Val Gln
 355 360 365
 Leu Asn Gln Ile Pro Val Val Asp Lys Gly Met Ala Val Leu Phe Asp
 370 375 380
 Glu Gln Ala Met Ser Asn Thr Leu Thr His Glu Asn Val Thr Ile Asp
 385 390 395 400
 Val Gln Leu Gly Leu Gly Asn Ala Ala Thr Ala Tyr Gly Cys Asp
 405 410 415
 Leu Ser Tyr Asp Tyr Val Arg Ile Asn Ala Ser Tyr Arg Thr
 420 425 430

(2) INFORMATION FOR SEQ ID NO:5245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 469 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

Asn Pro Ala Leu Thr Val Phe Ala Phe Ile Met Ile Ile Ser Ile Leu
 1 5 10 15
 Leu Ala Tyr Val Phe Lys Trp Leu Gly Leu Val Asp Asp Val Leu Leu

20					25					30					
Met	Val	Ile	Ile	Ile	Ser	Thr	Ile	Ser	Leu	Gly	Val	Val	Val	Pro	Thr
	35						40					45			
Leu	Lys	Glu	Met	Asn	Ile	Met	Arg	Thr	Thr	Ile	Gly	Gln	Phe	Ile	Leu
	50					55					60				
Leu	Val	Ala	Val	Leu	Ala	Asp	Leu	Val	Thr	Met	Ile	Leu	Leu	Thr	Val
	65					70					75				80
Tyr	Gly	Ala	Ile	Asn	Gly	Gln	Gly	Gly	Ser	Thr	Ile	Trp	Leu	Ile	Gly
				85					90					95	
Ile	Leu	Val	Val	Phe	Thr	Ala	Ile	Ser	Tyr	Ile	Leu	Gly	Val	Gln	Phe
			100					105					110		
Lys	Arg	Met	Ser	Phe	Leu	Gln	Lys	Leu	Met	Asp	Gly	Thr	Thr	Gln	Ile
		115					120					125			
Gly	Ile	Arg	Ala	Val	Phe	Ala	Leu	Ile	Ile	Leu	Leu	Val	Ala	Leu	Ala
	130					135					140				
Glu	Gly	Val	Gly	Ala	Glu	Asn	Ile	Leu	Gly	Ala	Phe	Leu	Ala	Gly	Val
	145					150					155				160
Val	Val	Ser	Leu	Leu	Asn	Pro	Asp	Glu	Glu	Met	Val	Glu	Lys	Leu	Asp
			165						170					175	
Ser	Phe	Gly	Tyr	Gly	Phe	Phe	Ile	Pro	Ile	Phe	Phe	Ile	Met	Xaa	Gly
			180					185					190		
Val	Asp	Leu	Asn	Ile	Pro	Ser	Leu	Ile	Lys	Glu	Pro	Lys	Leu	Leu	Ile
		195					200					205			
Ile	Ile	Pro	Ile	Leu	Ile	Val	Ala	Phe	Ile	Ile	Ser	Lys	Leu	Ile	Pro
	210					215					220				
Val	Met	Phe	Ile	Arg	Arg	Trp	Phe	Asp	Met	Lys	Thr	Thr	Ile	Ala	Ser
	225					230					235				240
Ala	Phe	Leu	Leu	Thr	Ser	Thr	Leu	Ser	Leu	Val	Ile	Ala	Ala	Ala	Lys
				245					250					255	
Ile	Ser	Glu	Arg	Leu	Asn	Ala	Ile	Ser	Ala	Glu	Thr	Ser	Gly	Ile	Leu
			260					265					270		
Ile	Leu	Ser	Ala	Val	Ile	Thr	Cys	Val	Phe	Val	Pro	Ile	Ile	Phe	Lys
	275						280					285			
Lys	Leu	Phe	Pro	Val	Pro	Asp	Glu	Phe	Asn	Arg	Lys	Ile	Glu	Val	Ser
	290					295					300				
Leu	Ile	Gly	Lys	Asn	Gln	Leu	Thr	Ile	Pro	Ile	Ala	Gln	Asn	Leu	Thr
	305					310					315				320
Ser	Gln	Leu	Tyr	Asp	Val	Thr	Leu	Tyr	Tyr	Arg	Lys	Asp	Leu	Ser	Asp
			325						330					335	
Arg	Arg	Gln	Leu	Ser	Asp	Asp	Ile	Thr	Met	Ile	Glu	Ile	Ala	Asp	Tyr
			340					345					350		

Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val
 355 360 365
 Val Cys Ala Thr Asn Asp Asp Asp Ile Asn Arg Lys Val Ala Lys Leu
 370 375 380
 Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr
 385 390 395 400
 Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser
 405 410 415
 Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn
 420 425 430
 Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln
 435 440 445
 Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe
 450 455 460
 Gly Gly Asp Ile Ile
 465

(2) INFORMATION FOR SEQ ID NO:5246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:

Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala
 1 5 10 15
 Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala
 20 25 30
 Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu
 35 40 45
 Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu
 50 55 60
 Asn Ile Tyr Arg Arg Leu Thr Asp Ser Glu Glu Gln Leu Lys Gly Glu
 65 70 75 80
 Asn Leu Ile Ile Ser Ala Thr Thr Glu Val Phe Lys Pro Ile Met Ser
 85 90 95
 Ser Thr Leu Val Thr Ile Ile Val Phe Leu Pro Leu Val Phe Val Ser
 100 105 110

Gly Ser Val Gly Glu Met Phe Arg Pro Phe Ala Leu Ala Ile Ala Phe
 115 120 125
 Ser Leu Leu Ala Ser Leu Leu Val Ser Ile Thr Leu Val Pro Ala Leu
 130 135 140
 Ala Ala Thr Leu Phe Lys Lys Gly Val Lys Arg Arg Asn Lys Gln His
 145 150 155 160
 Gln Glu Gly Leu Gly Val Val Ser Thr Thr Tyr Lys Lys Val Leu His
 165 170 175
 Trp Ser Leu Asn His Lys Trp Ile Val Ile Ile Leu Ser Thr Leu Ile
 180 185 190
 Leu Val Ala Thr Ile Val Phe Gly Gly Pro Arg Leu Gly Thr Ser Phe
 195 200 205
 Ile Ser Ala Gly Asp Asp Lys Phe Leu Ala Ile Thr Tyr Thr Pro Lys
 210 215 220
 Pro Gly Glu Thr Glu Gln Ala Val Leu Asn His Ala Lys Asp Val Glu
 225 230 235 240
 Lys Tyr Leu Lys Gln Lys Lys His Val Lys Thr Ile Gln Tyr Ser Ala
 245 250 255
 Gly Gly Ser Ser Pro Val Asp Pro Thr Gly Ser Thr Asn Ser Met Ala
 260 265 270
 Ile Met Val Glu Tyr Asp Asn Asp Thr Pro Asn Phe Asp Val Glu Ala
 275 280 285
 Asp Lys Val Ile Lys His Ala Asp Gly Phe Lys His Pro Gly Glu Trp
 290 295 300
 Lys Asn Gln Asp Leu Gly Thr Gly Ala Gly Asn Lys Ser Val Glu Val
 305 310 315 320
 Thr Val Lys Gly Pro Ser Met Asp Ala Ile Lys Ser Thr Val Lys Asp
 325 330 335
 Ile Glu Gln Lys Met Lys Gln Val Lys Gly Leu Ala Asn Val Lys Ser
 340 345 350
 Asp Leu Ser Gln Thr Tyr Asp Gln Tyr Glu Ile Lys Val Asp Gln Asn
 355 360 365
 Lys Ala Ala Glu Asn Gly Ile Ser Ala Ser Gln Leu Ala Met His Leu
 370 375 380
 Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly
 385 390 395 400
 Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala
 405 410

(2) INFORMATION FOR SEQ ID NO:5247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

Gly	Lys	Pro	Phe	Ile	Ile	Gly	Leu	Gly	Asp	Ile	Ile	Val	Lys	Lys	Leu	1	5	10	15
Thr	Thr	Ile	Leu	Phe	Gln	Tyr	Lys	Ile	Phe	Pro	Val	Leu	Met	Phe	Leu	20	25	30	
Val	Ser	Thr	Gly	Leu	Gly	Ile	Ile	Val	Ile	Thr	Gln	Asn	Ile	Leu	Ile	35	40	45	
Ala	Asp	Phe	Leu	Ala	Lys	Ile	Ile	Arg	His	Gln	Phe	Gln	Gly	Leu	Trp	50	55	60	
Ile	Val	Leu	Phe	Ile	Leu	Leu	Gly	Val	Leu	Leu	Leu	Arg	Ala	Thr	Val	65	70	75	
Gln	Phe	Leu	Asn	Gln	Trp	Leu	Gly	Asp	Thr	Leu	Ala	Phe	Lys	Val	Lys	85	90	95	
His	Met	Leu	Arg	Gln	Arg	Val	Ile	Tyr	Lys	Asn	Asn	Gly	His	Pro	Ile	100	105	110	
Gly	Glu	Gln	Met	Thr	Ile	Leu	Thr	Glu	Asn	Ile	Asp	Gly	Leu	Ala	Pro	115	120	125	
Phe	Tyr	Lys	Ser	Tyr	Leu	Pro	Gln	Val	Phe	Lys	Ser	Met	Met	Val	Pro	130	135	140	
Leu	Ile	Ile	Ile	Ile	Ala	Met	Phe	Phe	Ile	His	Phe	Asn	Thr	Ala	Leu	145	150	155	
Ile	Met	Leu	Ile	Thr	Ala	Pro	Phe	Ile	Pro	Leu	Phe	Tyr	Ile	Ile	Phe	165	170	175	
Gly	Leu	Lys	Thr	Arg	Asp	Glu	Ser	Lys	Asp	Gln	Met	Thr	Tyr	Leu	Asn	180	185	190	
Gln	Phe	Ser	Gln	Arg	Phe	Leu	Asn	Ile	Ala	Lys	Gly	Leu	Val	Thr	Leu	195	200	205	
Lys	Leu	Phe	Asn	Arg	Thr	Glu	Gln	Thr	Glu	Lys	His	Ile	Tyr	Asp	Asp	210	215	220	
Ser	Thr	Gln	Phe	Arg	Thr	Leu	Thr	Met	Arg	Ile	Leu	Arg	Ser	Ala	Phe	225	230	235	
Leu	Ser	Gly	Leu	Met	Leu	Glu	Phe	Ile	Ser	Met	Leu	Gly	Ile	Gly	Leu	245	250	255	
Val	Ala	Leu	Glu	Ala	Thr	Leu	Ser	Leu	Val	Val	Phe	His	Asn	Ile	Asp	260	265	270	

Phe Lys Thr Ala Ala Ile Ala Ile Ile Leu Ala Pro Glu Phe Tyr Asn
275 280 285
Ala Ile Lys Asp Leu Gly Gln Ala Phe His Thr GlyLys Gln Ser Glu
290 295 300
Gly Ala Ser Asp Val Val Phe Glu Phe Leu Glu Gln Pro Asn Tyr Asn
305 310 315 320
Asn Glu Phe Leu Leu Lys Tyr Glu Glu Asn Gln Lys Pro Phe Ile Gln
325 330 335
Leu Thr Asp Ile Ser Phe Arg Tyr Asp Asp Ser Asp Arg Leu Val Leu
340 345 350
Asn Asp Leu Asn Leu Glu Ile Phe Lys Gly Asp Gln Ile Ala Leu Val
355 360 365
Gly Pro Ser Gly Ala Gly Lys Ser Thr Leu Thr His Leu Ile Ala Gly
370 375 380
Val Tyr Gln Pro Thr Ile Gly Thr Ile Ser Thr Asn Gln Arg Asp Leu
385 390 395 400
Asn Ile Gly Ile Leu Ser Gln Gln Pro Tyr Ile Phe Ser Ala Ser Ile
405 410 415
Lys Glu Asn Ile Thr Met Phe Lys Asp Ile Glu Asn Asn Thr Ile Glu
420 425 430
Glu Val Leu Asp Glu Val Gly Leu Leu Asp Lys Val Gln Ser PheThr
435 440 445
Lys Gly Ile Asn Thr Ile Ile Gly Glu Gly Gly Glu Met Leu Ser Gly
450 455 460
Gly Gln Met Arg Arg Ile Glu Leu Qs Arg Leu Leu Val Met Lys Pro
465 470 475 480
Asp Leu Val Ile Phe Asp Glu Pro Ala Thr Gly Leu Asp Ile Gln Thr
485 490 495
Glu His Met Ile Gln Asn Val Leu Phe Gln His Phe Lys Asp Thr Thr
500 505 510
Met Ile Val Ile Ala His Arg Asp Asn Thr Ile Arg His Leu Gln Arg
515 520 525
Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile
530 535 540
Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu
545 550 555

(2) INFORMATION FOR SEQ ID NO:5248:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

Val	Trp	Lys	Leu	Lys	Met	Arg	Trp	Ile	Lys	Arg	Lys	Lys	Lys	Asn	Phe	
1				5					10					15		
Leu	Asn	Ser	Lys	Phe	Asn	Phe	Asn	Asn	Gly	Lys	Ile	Ala	Thr	Tyr	Leu	
			20					25					30			
Tyr	Lys	Glu	Arg	Thr	Ala	Met	Trp	Asn	Lys	Asn	Arg	Leu	Thr	Gln	Met	
		35					40					45				
Leu	Ser	Ile	Glu	Tyr	Pro	Ile	Ile	Gln	Ala	Gly	Met	Ala	Gly	Ser	Thr	
	50					55					60					
Thr	Pro	Lys	Leu	Val	Ala	Ser	Val	Ser	Asn	Ser	Gly	Gly	Leu	Gly	Thr	
65					70					75					80	
Ile	Gly	Ala	Gly	Tyr	Phe	Asn	Thr	Gln	Gln	Leu	Glu	Asp	Glu	Ile	Asp	
				85					90					95		
Tyr	Val	Arg	Gln	Leu	Thr	Ser	Asn	Ser	Phe	Gly	Val	Asn	Val	Phe	Val	
			100					105					110			
Pro	Ser	Gln	Gln	Ser	Tyr	Thr	Ser	Ser	Gln	Ile	Glu	Asn	Met	Asn	Ala	
		115					120					125				
Trp	Leu	Lys	Pro	Tyr	Arg	Arg	Ala	Leu	His	Leu	Glu	Glu	Pro	Val	Val	
	130					135					140					
Lys	Ile	Thr	Glu	Glu	Gln	Gln	Phe	Lys	Cys	His	Ile	Asp	Thr	Ile	Ile	
145					150					155					160	
Lys	Lys	Gln	Val	Pro	Val	Cys	Cys	Phe	Thr	Phe	Gly	Ile	Pro	Ser	Glu	
			165						170					175		
Gln	Ile	Ile	Ser	Arg	Leu	Lys	Ala	Ala	Asn	Val	Lys	Leu	Ile	Gly	Thr	
			180					185						190		
Ala	Thr	Ser	Val	Asp	Glu	Ala	Ile	Ala	Asn	Glu	Lys	Ala	Gly	Met	Asp	
		195					200					205				
Ala	Ile	Val	Ala	Gln	Gly	Ser	Glu	Ala	Gly	Gly	His	Arg	Gly	Ser	Phe	
	210					215					220					
Leu	Lys	Pro	Lys	Asn	Gln	Leu	Pro	Met	Val	Gly	Thr	Ile	Ser	Leu	Val	
225					230					235					240	
Pro	Gln	Ile	Val	Asp	Val	Val	Ser	Ile	Pro	Val	Ile	Ala	Ala	Gly	Gly	
			245						250					255		
Ile	Met	Asp	Gly	Arg	Gly	Val	Leu	Ala	Ser	Ile	Val	Leu	Gly	Ala	Glu	
		260					265						270			
Gly	Val	Gln	Met	Gly	Thr	Ala	Phe	Leu	Thr	Ser	Gln	Asp	Ser	Asn	Ala	

Thr Thr Thr Asn Gln Ala Asn Thr Pro Ala Thr Thr Gln Ser Ser Asn
 130 135 140
 Thr Asn Ala Glu Glu Leu Val Asn Gln Thr Ser Asn Glu Thr Thr Ser
 145 150 155 160
 Asn Asp Thr Asn Thr Val Ser Ser Val Asn Ser Pro Gln Asn Ser Thr
 165 170 175
 Asn Ala Glu Asn Val Ser Thr Thr Gln Asp Thr Ser Thr Glu Ala Thr
 180 185 190
 Pro Ser Asn Asn Glu Ser Ala Pro Gln Ser Thr Asp Ala Ser Asn Lys
 195 200 205
 Asp Val Val Asn Gln Ala Val Asn Thr Ser Ala Pro Arg Met Arg Ala
 210 215 220
 Phe Ser Leu Ala Ala Val Ala Ala Asp Ala Pro Val Ala Gly Thr Asp
 225 230 23 240
 Ile Thr Asn Gln Leu Thr Asn Val Thr Val Gly Ile Asp Ser Gly Thr
 245 250 255
 Thr Val Tyr Pro His Gln Ala Gly Tyr Val Lys Leu Asn Tyr Gly Phe
 260 265 270
 Ser Val Pro Asn Ser Ala Val Lys Gly Asp Thr Phe Lys Ile Thr Val
 275 280 285
 Pro Lys Glu Leu Asn Leu Asn Gly Val Thr Ser Thr Ala Lys ValPro
 290 295 300
 Pro Ile Met Ala Gly Asp Gln Val Leu Ala Asn Gly Val Ile Asp Ser
 305 310 315 320
 Asp Gly Asn Val Ile Tyr Thr Phe Thr Asp Tyr Val Asn Thr Lys Asp
 325 330 335
 Asp Val Lys Ala Thr Leu Thr Met Pro Ala Tyr Ile Asp Pro Glu Asn
 340 345 350
 Val Lys Lys Thr Gly Asn Val Thr Leu Ala Thr Gly Ile Gly Ser Thr
 355 360 365
 Thr Ala Asn Lys Thr Val Leu Val Asp Tyr Glu Lys Tyr Gly Lys Phe
 370 375 380
 Tyr Asn Leu Ser Ile Lys Gly Thr Ile Asp Gln Ile Asp Lys Thr Asn
 385 390 395 400
 Asn Thr Tyr Arg Gln Thr Ile Tyr Val Asn Pro Ser Gly Asp Asn Val
 405 410 415
 Ile Ala Pro Val Leu Thr Gly Asn Leu Lys Pro Asn Thr Asp Ser Asn
 420 425 430
 Ala Leu Ile Asp Gln Gln Asn Thr Ser Ile Lys Val Tyr Lys Val Asp
 435 440 445

Asn Ala Ala Asp Leu Ser Glu Ser Tyr Phe Val Asn Pro Glu Asn Phe
 450 455 460
 Glu Asp Val Thr Asn Ser Val Asn Ile Thr Phe Po Asn Pro Asn Gln
 465 470 475 480
 Tyr Lys Val Glu Phe Asn Thr Pro Asp Asp Gln Ile Thr Thr Pro Tyr
 485 490 495
 Ile Val Val Val Asn Gly His Ile Asp Pro Asn Ser Lys Gly Asp Leu
 500 505 510
 Ala Leu Arg Ser Thr Leu Tyr Gly Tyr Asn Ser Asn Ile Ile Trp Arg
 515 520 525
 Ser Met Ser Trp Asp Asn Glu Val Ala Phe Asn Asn Gly Ser Gly Ser
 530 535 540
 Gly Asp Gly Ile Asp Lys Pro Val Val Pro Glu Gln Pro Asp Glu Pro
 545 550 555 560
 Gly Glu Ile Glu Pro Ile Pro Glu Asp Ser Asp Ser Asp Pro Gly Ser
 565 570 575
 Asp Ser Gly Ser Asp Ser Asn Ser Asp Ser Gly Ser Asp Ser Gly Ser
 580 585 590
 Asp Ser Thr Ser Asp Ser Gly Ser Asp Ser Ala Ser Asp Ser Asp Ser
 595 600 605
 Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Ala Ser Asp Ser
 610 615 620
 Asp Ser Ala Ser Asp Ser Asp Ser Asp Asn Asp Ser Asp Ser Asp Ser
 625 630 635 640
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 645 650 655
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 660 665 670
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 675 680 685
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 690 695 700
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 705 710 715 720
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 725 730 735
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 740 745 750
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 755 760 765
 Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp Ser

770		775		780
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser				
785		790		800
Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser				
	805		810	815
Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser				
	820		825	830
Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Gly Ser				
	835		840	845
Asp Ser Asp Ser Ser Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser				
	850		855	860
Asp Ser Glu Ser Val Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro				
	865	870	875	880
Lys Asn Gly Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys				
	885		890	895
Glu Pro Leu Pro Asp Thr Gly Ser Glu Asp Glu Ala Asn Thr Ser Leu				
	900		905	910
Ile Trp Gly Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg				
	915		920	925
Lys Lys Glu Asn Lys Asp Lys Lys				
	930		935	

(2) INFORMATION FOR SEQ ID NO:5250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala		
1	5	10
Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro		
	20	25
Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu		
	35	40
Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys		
	50	55
Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys		
	65	70
		75
		80

Phe Lys Ser Glu Pro Pro Val Glu Lys His Glu Leu Thr Gly Thr Ile
115 120 125
Glu Glu Ser Asn Asp Ser Lys Pro Ile Asp Phe Glu Tyr His Thr Ala
130 135 140
Val Glu Gly Ala Glu Gly His Ala Glu Gly Thr Ile Glu Thr Glu Glu
145 150 155 160
Asp Ser Ile His Val Asp Phe Glu Glu Ser Thr His Glu Asn Ser Lys
165 170 175
His His Ala Asp Val Val Glu Tyr Glu Glu Asp Thr Asn Pro Gly Gly
180 185 190
Gly Gln Val Thr Thr Glu Ser Asn Leu Val Glu Phe Asp Glu Asp Ser
195 200 205
Thr Lys Gly Ile Val Thr Gly Ala Val Ser Asp His Thr Thr Ile Glu
210 215 220
Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn Leu IleGlu Leu Val Asp
225 230 235 240
Glu Leu Pro Glu Glu His Gly Gln Ala Gln Gly Pro Ile Glu Glu Ile
245 250 255
Thr Glu Asn Asn His His Ile Ser His Ser Gly Leu Gly Thr Glu Asn
260 265 270
Gly His Gly Asn Tyr Gly Val Ile Glu Glu Ile Glu Glu Asn Ser His
275 280 285
Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu Gly Gly Gln Asn Ser Gly
290 295 300
Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu Asp Lys Pro Lys Tyr Glu
305 310 315 320
Gln Gly Gly Asn Ile Val Asp Ile Asp Phe Asp Ser Val Pro Gln Ile
325 330 335
His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys
340 345 350
Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe
355 360 365
Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu IleIle
370 375 380
Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His
385 390 395 400
Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His
405 410 415
Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val
420 425 430
Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro

435	440	445
Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro		
450	455	460
Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala		
465	470	475
Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val		
485	490	495
Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro		
500	505	510
Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly		
515	520	525
Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile		
530	535	540
Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys LysAsn His Lys Ala		
545	550	555

(2) INFORMATION FOR SEQ ID NO:5252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu		
1	5	10
Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val		
20	25	30
Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn		
35	40	45
Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp		
50	55	60
Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu		
65	70	75
Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro		
85	90	95
Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Glu Ile Ile		
100	105	110
Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys		
115	120	125

Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr
 130 135 140
 Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu
 145 150 155 160
 Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg
 165 170 175
 Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys
 180 185 190
 Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln
 195 200 205
 Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys
 210 215 220
 Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser
 225 230 235 240
 Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala
 245 250

(2) INFORMATION FOR SEQ ID NO:5253:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr
 1 5 10 15
 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
 20 25 30
 Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu
 35 40 45
 Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser
 50 55 60
 Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp
 65 70 75 80
 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser
 85 90 95
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys
 100 105 110

Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys
115 120 125

Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser
130 135 140

Glu Ile Lys Pro Arg Met Lys Arg Ser Met Thr Leu Gln Gln Leu Gln
145 150 155 160

Arg Lys Lys

(2) INFORMATION FOR SEQ ID NO:5254:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1027 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

Ile Leu His Leu Lys Gly Asp Ile Ile Val Lys Asn Asn Leu Arg Tyr
1 5 10 15

Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
20 25 30

Met Ile Val Val Gly Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu
35 40 45

Gln Lys Thr Thr Thr Val Glu Glu Asn Gly Asn Ser Ala Thr Asp Asn
50 55 60

Lys Thr Ser Glu Thr Gln Thr Thr Ala Thr Asn Val Asn His Ile Glu
65 70 75 80

Glu Thr Gln Ser Tyr Asn Ala Thr Val Thr Gln Gln Pro Ser Asn Ala
85 90 95

Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Ala Val Gln Ala Pro Gln
100 105 110

Thr Ala Gln Pro Ala Asn Ile Glu Thr Val Lys Glu Glu Val Val Lys
115 120 125

Glu Glu Ala Lys Pro Gln Val Lys Glu Thr Thr Gln Ser Gln Asp Asn
130 135 140

Ser Gly Asp Gln Arg Gln Val Asp Leu Thr Pro Lys Lys Ala Thr Gln
145 150 155 160

Asn Gln Val Ala Glu Thr Gln Val Glu Val Ala Gln Pro Arg Thr Ala
165 170 175

Ser Glu Ser Lys Pro Arg Val Thr Arg Ser Ala Asp Val Ala Glu Ala

180					185					190					
Lys	Glu	Ala	Ser	Asn	Ala	Lys	Val	Glu	Thr	Gly	Thr	Asp	Val	Thr	Ser
		195						200				205			
Lys	Val	Thr	Val	Glu	Ile	Gly	Ser	Ile	Glu	Gly	His	Asn	Asn	Thr	Asn
	210					215					220				
Lys	Val	Glu	Pro	His	Ala	Gly	Gln	Arg	Ala	Val	Leu	Lys	Trp	Lys	Leu
225					230					235					240
Lys	Phe	Glu	Asn	Gly	Leu	His	Gln	Gly	Asp	Tyr	Phe	Asp	Phe	Thr	Leu
				245					250					255	
Ser	Asn	Asn	Val	Asn	Thr	His	Gly	Val	Ser	Thr	Ala	Arg	Lys	Val	Pro
			260					265					270		
Glu	Ile	Lys	Asn	Gly	Ser	Val	Val	Met	Ala	Thr	Gly	Glu	Val	Leu	Glu
		275					280					285			
Gly	Gly	Lys	Ile	Arg	Tyr	Thr	Phe	Thr	Asn	Asp	Ile	Glu	Asp	Lys	Val
	290					295					300				
Asp	Val	Thr	Ala	Glu	Leu	Glu	Ile	Asn	Leu	Phe	Ile	Asp	Pro	Lys	Thr
305					310					315					320
Val	Gln	Thr	Asn	Gly	Asn	Gln	Thr	Ile	Thr	Ser	Thr	Leu	Asn	Glu	Glu
				325					330					335	
Gln	Thr	Ser	Lys	Glu	Leu	Asp	Val	Lys	Tyr	Lys	Asp	Gly	Ile	Gly	Asn
			340					345					350		
Tyr	Tyr	Ala	Asn	Leu	Asn	Gly	Ser	Ile	Glu	Thr	Phe	Asn	Lys	Ala	Asn
		355					360					365			
Asn	Arg	Phe	Ser	His	Val	Ala	Phe	Ile	Lys	Pro	Asn	Asn	Gly	Lys	Thr
	370					375					380				
Thr	Ser	Val	Thr	Val	Thr	Gly	Thr	Leu	Met	Lys	Gly	Ser	Asn	Gln	Asn
385					390					395					400
Gly	Asn	Gln	Pro	Lys	Val	Arg	Ile	Phe	Gln	Tyr	Leu	Gly	Asn	Asn	Glu
				405					410					415	
Asp	Ile	Ala	Lys	Ser	Val	Tyr	Ala	Asn	Thr	Thr	Asp	Thr	Ser	Lys	Phe
			420					425					430		
Lys	Glu	Val	Thr	Ser	Asn	Met	Ser	Gly	Asn	Leu	Asn	Leu	Gln	Asn	Asn
	435						440					445			
Gly	Ser	Tyr	Ser	Leu	Asn	Ile	Glu	Asn	Leu	Asp	Lys	Thr	Tyr	Val	Val
	450					455					460				
His	Tyr	Asp	Gly	Glu	Tyr	Leu	Asn	Gly	Thr	Asp	Glu	Val	Asp	Phe	Arg
465					470					475					480
Thr	Gln	Met	Val	Gly	His	Pro	Glu	Gln	Leu	Tyr	Lys	Tyr	Tyr	Tyr	Asp
				485				490					495		
Arg	Gly	Tyr	Thr	Leu	Thr	Trp	Asp	Asn	Gly	Leu	Val	Leu	Tyr	Ser	Asn
			500					505					510		

3000

Lys Ala Asn Gly Asn Glu Lys Asn Gly Pro Ile Ile Gln Asn Asn Lys
 515 520 525
 Phe Glu Tyr Lys Glu Asp Thr Ile Lys Glu Thr Leu Thr Gly Gln Tyr
 530 535 540
 Asp Lys Asn Leu Val Thr Thr Val Glu Glu Glu Tyr Ap Ser Ser Thr
 545 550 555 560
 Leu Asp Ile Asp Tyr His Thr Ala Ile Asp Gly Gly Gly Gly Tyr Val
 565 570 575
 Asp Gly Tyr Ile Glu Thr Ile Glu Glu Thr Asp Ser Ser Ala Ile Asp
 580 585 590
 Ile Asp Tyr His Thr Ala Val Asp Ser Glu Ala Gly His Val Gly Gly
 595 600 605
 Tyr Thr Glu Ser Ser Glu Glu Ser Asn Pro Ile Asp Phe Glu Glu Ser
 610 615 620
 Thr His Glu Asn Ser Lys His His Ala Asp Val Val Glu Tyr Glu Glu
 625 630 635 640
 Asp Thr Asn Pro Gly Gly Gly Gln Val Thr Thr Glu Ser Asn Leu Val
 645 650 655
 Glu Phe Asp Glu Glu Ser Thr Lys Gly Ile Val Thr Gly Ala Val Ser
 660 665 670
 Asp His Thr Thr Val Glu Asp Thr Lys Glu Tyr Thr Thr Glu Ser Asn
 675 680 685
 Leu Ile Glu Leu Val Asp Glu Leu Pro Glu Glu His Gly Gln AlaGln
 690 695 700
 Gly Pro Val Glu Glu Ile Thr Lys Asn Asn His His Ile Ser His Ser
 705 710 715 720
 Gly Leu Gly Thr Glu Asn Gly His Gly Asn Tyr Asp Val Ile Glu Glu
 725 730 735
 Ile Glu Glu Asn Ser His Val Asp Ile Lys Ser Glu Leu Gly Tyr Glu
 740 745 750
 Gly Gly Gln Asn Ser Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Glu
 755 760 765
 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Val Asp Ile Asp Phe
 770 775 780
 Asp Ser Val Pro Gln Ile His Gly Gln Asn Lys Gly Asn Gln Ser Phe
 785 790 795 800
 Glu Glu Asp Thr Glu Lys Asp Lys Pro Lys Tyr Glu His Gly Gly Asn
 805 810 815
 Ile Ile Asp Ile Asp Phe Asp Ser Val Pro His Ile His Gly Phe Asn
 820 825 830

Lys His Thr Glu Ile Ile Glu Glu Asp Thr Asn Lys Asp Lys Pro Ser
 835 840 845
 Tyr Gln Phe Gly Gly His Asn Ser Val Asp Phe Glu Glu Asp Thr Leu
 850 855 860
 Pro Lys Val Ser Gly Gln Asn Glu Gly Gln Gln Trp Ile Glu Glu Asp
 865 870 875 880
 Thr Thr Pro Pro Ile Val Pro Pro Thr Pro Pro Thr Pro Glu Val Pro
 885 890 895
 Ser Glu Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu
 900 905 910
 Pro Glu Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu
 915 920 925
 Thr Pro Thr Pro Pro Thr Pro Glu Val Pro Ala Glu Pro Gly Lys Pro
 930 935 940
 Val Pro Pro Ala Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu
 945 950 955 960
 Gln Gly Lys Val Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys
 965 970 975
 Ala Val Ala Pro Thr Lys Lys Pro Gln Ser Lys Lys Ser Glu Leu Pro
 980 985 990
 Glu Thr Gly Gly Glu Glu Ser Thr Asn Lys Gly Met Leu Phe Gly Gly
 995 1000 1005
 Leu Phe Ser Ile Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn
 1010 1015 1020
 His Lys Ala
 1025

(2) INFORMATION FOR SEQ ID NO:5255:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

Gly Glu Lys Cys Met Phe Leu Ala Trp Asn Glu Ile Arg Arg Asn Lys
 1 5 10 15
 Leu Lys Phe Gly Leu Ile Ile Gly Val Leu Thr Met Ile Ser Tyr Leu
 20 25 30
 Leu Phe Leu Leu Ser Gly Leu Ala Asn Gly Leu Ile Asn Met Asn Lys

35		40		45
Glu Gly Ile Asp Lys Trp Gln Ala Asp Ala Ile Val Leu Asn Lys Asp				
50		55		60
Ala Asn Gln Thr Val Gln Gln Ser Val Phe Asn Lys Lys Asp Ile Glu				
65		70		75 80
Asn Lys Tyr Lys Lys Gln Ala Thr Leu Lys Gln Thr Gly Glu Ile Val				
	85		90	95
Ser Asn Gly His Gln Lys Asp Asn Val Leu Val Phe Gly Val Glu Lys				
	100		105	110
Ser Ser Phe Leu Val Pro Ser Leu Ile Glu Gly His Lys Ala Thr Lys				
	115		120	125
Asp Asn Glu Val Leu Ala Asp Glu Thr Leu Lys Asn Lys Gly Leu Lys				
	130		135	140
Leu Gly Asp Thr Leu Ser Leu Ser Xaa Xaa Arg				
145		150		155